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OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 11:34:17 ; Search time 56 Seconds
(without alignments)
165.519 Million cell updates/sec

Title: US-09-913-325-5

Perfect score: 21
Sequence: 1 atgtctgagaccgtctgctc 21

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 569978 seqs, 220591566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/prodata/2/ina/5A COMB.seq:*
- 2: /cgn2_6/prodata/2/ina/5B COMB.seq:*
- 3: /cgn2_6/prodata/2/ina/6A COMB.seq:*
- 4: /cgn2_6/prodata/2/ina/6B COMB.seq:*
- 5: /cgn2_6/prodata/2/ina/6C COMB.seq:*
- 6: /cgn2_6/prodata/2/ina/6D COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	21	100.0	195	2	US-08-485-657A-14
C 2	21	100.0	195	4	US-09-366-380-14
C 3	21	100.0	195	5	PCT-US95-02303-14
C 4	21	100.0	1648	4	US-09-659-791A-3
C 5	21	100.0	1651	4	US-09-659-791A-13
C 6	21	100.0	7610	4	US-09-659-791A-12
C 7	19.4	92.4	181	2	US-08-485-657A-19
C 8	19.4	92.4	181	4	US-09-366-380-19
C 9	19.4	92.4	181	5	PCT-US95-02303-18
C 10	15.2	72.4	6671	1	US-08-280-443-1
C 11	15.2	72.4	6671	1	US-08-457-459-1
C 12	15.2	72.4	6671	1	US-08-555-678-1
C 13	15.2	72.4	6671	5	PCT-US95-02275-1
C 14	15.2	72.4	6756	1	US-08-151-574-31
C 15	15.2	72.4	6756	2	US-08-419-448-31
C 16	15.2	72.4	6756	4	US-09-233-510-31
C 17	14.8	70.5	1438	3	US-09-187-331-4
C 18	14.8	70.5	1438	4	US-09-470-946-4
C 19	14.8	70.5	3563	3	US-09-041-886-20
C 20	14.8	70.5	3596	2	US-08-779-801-5
C 21	14.8	70.5	3596	4	US-09-298-441-5
C 22	14.8	70.5	4403765	3	US-09-103-840A-2
C 23	14.8	70.5	4411529	3	US-09-103-840A-1
C 24	14.6	69.5	885	4	US-09-252-991A-2618
C 25	14.6	69.5	1080	4	US-09-252-991A-2217
C 26	14.6	69.5	1219	4	US-09-192-012-1
C 27	14.6	69.5	2139	4	US-09-252-991A-2295

ALIGNMENTS

RESULT 1

US-08-485-657A-14/c
; Sequence 14, Application US/08485657A
; Patent No. 5942389
; GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J
; APPLICANT: Gudkov, Andrei
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,657A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5942389nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-485-657A-14

Query Match 100.0%; Score 21; DB 2; Length 195;

Best Local Similarity 100.0%; Pred. No. 0.05; Mismatches 0; Gaps 0;

Matches 21; Conservative 0; Indels 0; Gaps 0;

1 ATTGTCGAGACCGTCGTC 21

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Db      153 ATTGTCTGAGACCGTCTGGTC 133

RESULT 2
US-09-366-380-14/c
; Sequence 14, Application US/09366380
; Patent No. 6541603
; GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J
; APPLICANT: Gudkov, Andrei
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/366,380
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/199,900
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6541603nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-366-380-14

Query Match      100.0%; Score 21; DB 4; Length 195;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATTGTCTGAGACCGTCTGGTC 21
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Db      153 ATTGTCTGAGACCGTCTGGTC 133

RESULT 3
PCT-US95-02303-14/c
; Sequence 14, Application PC/TUS9502303
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 25
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:

US-09-659-791A-13/c
; Sequence 13, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Preier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 13
; LENGTH: 1651
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)...(1545)
US-09-659-791A-13

Query Match      100.0%; Score 21; DB 4; Length 1651;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATTGTCTGAGACCGTCTGGTC 21
      |||||||||||||||||||
Db      139 ATTGTCTGAGACCGTCTGGTC 119

RESULT 4
US-09-659-791A-3/c
; Sequence 3, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Preier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 3
; LENGTH: 1648
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (53)...(1402)
US-09-659-791A-3

Query Match      100.0%; Score 21; DB 4; Length 1648;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATTGTCTGAGACCGTCTGGTC 21
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Db      139 ATTGTCTGAGACCGTCTGGTC 119

RESULT 5
US-09-659-791A-13/c
; Sequence 13, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Preier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 13
; LENGTH: 1651
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)...(1545)
US-09-659-791A-13

Query Match      100.0%; Score 21; DB 4; Length 1651;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ATTGTCTGAGACCGTCTGGTC 21
Db 282 ATTGTCTGAGACCGTCTGGTC 262

RESULT 6
US-09-659-791A-12/c
; Sequence 12, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 12
; LENGTH: 7610
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: unsure
; LOCATION: 5461
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 5462
; OTHER INFORMATION: unknown
US-09-659-791A-12

Query Match 100.0%; Score 21; DB 4; Length 7610;
Best Local Similarity 100.0%; Pred. No. 0.093; 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0

QY 1 ATTGTCTGAGACCGTCTGGTC 21
Db 5624 ATTGTCTGAGACCGTCTGGTC 5604

RESULT 7
US-08-485-657A-19/c
; Sequence 19, Application US/08485657A
; Patent No. 5942389
; GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J
; APPLICANT: Gudkov, Andrei
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,657A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5942389nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001

TELEFAX: 312-913-0002
TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-485-657A-19

Query Match 92.4%; Score 19.4; DB 2; Length 181;
Best Local Similarity 95.2%; Pred. No. 0.34; 1; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 1

QY 1 ATTGTCTGAGACCGTCTGGTC 21
Db 139 ATGGTCTGAGACCGTCTGGTC 119

RESULT 8
US-09-366-380-19/c
; Sequence 19, Application US/09366380
; Patent No. 6541603
; GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J
; APPLICANT: Gudkov, Andrei
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/366,380
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/199,900
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6541603nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-366-380-19

Query Match 92.4%; Score 19.4; DB 4; Length 181;
Best Local Similarity 95.2%; Pred. No. 0.34; 1; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 1

QY 1 ATTGTCTGAGACCGTCTGGTC 21
Db 139 ATGGTCTGAGACCGTCTGGTC 119

Db 139 ATGGCTGAGACCGCTGCTGTC 119

RESULT 9

PCT-US95-02303-18/c

Sequence 18, Application PC/TUS9502303

GENERAL INFORMATION:

APPLICANT: Genes and Genetic Elements Associated

TITLE OF INVENTION: with sensitivity to Cisplatin

NUMBER OF SEQUENCES: 25

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/02303

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 181 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

PCT-US95-02303-18

Query Match 92.4%; Score 19.4; DB 5; Length 181;

Best Local Similarity 95.2%; Pred. No. 0.34; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 1;

Qy 1 ATTGCTGAGACCGCTGCTGTC 21

Db 139 ATGGCTGAGACCGCTGCTGTC 119

RESULT 10

US-08-280-443-1/c

Sequence 1, Application US/08280443

Patent No. 5643778

GENERAL INFORMATION:

APPLICANT: Nishikura, Kazuko

TITLE OF INVENTION: RNA Editing Enzyme and Methods of Use

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Cntr, P.O. Box 457

CITY: Spring House

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/280,443

FILING DATE: 17-FEB-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/197,794

FILING DATE: 17-FEB-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/280,443

FILING DATE: 25-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: WST49AUSA

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9206

TELEFAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 6671 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: unknown

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 155..3832

US-08-457-459-1

Query Match 72.4%; Score 15.2; DB 1; Length 6671;

Best Local Similarity 85.0%; Pred. No. 98;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TTGCTGAGACCGCTGCTGTC 21

Db 808 TTGGCTATGACCGCTGCTGTC 789

RESULT 11

US-08-457-459-1/c

Sequence 1, Application US/08457459

Patent No. 5677428

GENERAL INFORMATION:

APPLICANT: Nishikura, Kazuko

TITLE OF INVENTION: RNA Editing Enzyme and Methods of Use

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Cntr, P.O. Box 457

CITY: Spring House

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/457,459

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/197,794

FILING DATE: 17-FEB-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/280,443

FILING DATE: 25-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: WST49CUSA

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9206

TELEFAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 6671 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: unknown

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 155..3832

US-08-457-459-1

Query Match 72.4%; Score 15.2; DB 1; Length 6671;

Best Local Similarity 85.0%; Pred. No. 98;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;


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;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
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;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/151,574
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/688,578
;; FILING DATE: 24-MAY-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Murashige, Kate H.
;; REGISTRATION NUMBER: 29,959
;; REFERENCE/DOCKET NUMBER: 24615-20026.00
;; TELEPHONE: 415-327-7250
;; INFORMATION FOR SEQ ID NO: 31:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6756 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Aspergillus ficuum (Aspergillus niger)
;; STRAIN: NRRL 3135
;; IMMEDIATE SOURCE:
;; LIBRARY: lambda AF
;; CLONE: pAF2-3, pAF2-6, pAF2-7
;; FEATURE:
;; NAME/KEY: exon
;; LOCATION: 210..253
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 254..355
;; FEATURE:
;; NAME/KEY: exon
;; LOCATION: 356..1715
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: join(210..253, 356..1715)
;; OTHER INFORMATION: /codon_start= 210
;; OTHER INFORMATION: /product= "Phytase"
;; FEATURE:
;; NAME/KEY: sig_peptide
;; LOCATION: 210..380
;; FEATURE:
;; NAME/KEY: mat_peptide
;; LOCATION: 381..1712
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;; OTHER INFORMATION: /function= "inositol phosphate"
;; OTHER INFORMATION: phosphatase
;; OTHER INFORMATION: /product= "Phytase"
;; OTHER INFORMATION: /evidence= EXPERIMENTAL
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;; US-08-151-574-31
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;; Query Match 72.4%; Score 15.2; DB 1; Length 6756;
;; Best Local Similarity 85.0%; Pred. No. 98;
;; Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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;; QY 2 TTGTCTGAGACCGTCTGGTC 21
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;; DB 130 TTATATGAGACCGTCCGGTC 149
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;; RESULT 15
;; US-08-419-448-31
;; Sequence 31, Application US/08419448
;;
;; Patent No. 5863533
;; GENERAL INFORMATION:
;; APPLICANT: Robert F.M. Van Gorkom
;; APPLICANT: Willem Van Hartingsveldt
;; APPLICANT: Petrus A. Van Paridon
;; APPLICANT: Annemarie E. Veenstra
;; APPLICANT: Rudolf G.M. Luttin
;; APPLICANT: Gerardus Seltin
;; TITLE OF INVENTION: Cloning and Expression of Microbial
;; NUMBER OF SEQUENCES: 52
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Morrison & Foerster
;; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20006-1888
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/419,448
;; FILING DATE: 10-APR-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Murashige, Kate H.
;; REGISTRATION NUMBER: 29,959
;; REFERENCE/DOCKET NUMBER: 24615-20026.10
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-887-1500
;; INFORMATION FOR SEQ ID NO: 31:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6756 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Aspergillus ficuum (Aspergillus niger)
;; STRAIN: NRRL 3135
;; IMMEDIATE SOURCE:
;; LIBRARY: lambda AF
;; CLONE: pAF2-3, pAF2-6, pAF2-7
;; FEATURE:
;; NAME/KEY: exon
;; LOCATION: 210..253
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 254..355
;; FEATURE:
;; NAME/KEY: exon
;; LOCATION: 356..1715
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: join(210..253, 356..1715)
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;; OTHER INFORMATION: /product= "Phytase"
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;; OTHER INFORMATION: /product= "Phytase"
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US-08-419-448-31

Query Match 72.4%; Score 15.2; DB 2; Length 6756;
Best Local Similarity 85.0%; Pred. No. 98;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 130 TTATGAGACCGTCCGTC 149

Search completed: January 21, 2004, 13:11:48;
Job time : 63 secs

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 10:07:51 : Search time 799.5 Seconds
(without alignments)
1074.549 Million cell updates/sec

Title: US-09-913-325-5
Perfect score: 21
Sequence: 1 attgtctgagaccgtctggtc 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

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C 3	21	100.0	482	6	BD117323 EST and e
C 4	21	100.0	491	6	BD027496 Sequence
C 5	21	100.0	512	6	BD071299 Sequence
C 6	21	100.0	1589	6	AX600212 Sequence
C 7	21	100.0	1648	6	AR208704 Sequence
C 8	21	100.0	1648	9	HUMTRPM2A
C 9	21	100.0	1651	6	A21577 blood plas
C 10	21	100.0	1651	6	AR208714 Sequence
C 11	21	100.0	1651	9	HUMCLI
C 12	21	100.0	1658	9	BC019588 Homo sapi
C 13	21	100.0	1676	9	HSCSP40
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C 18	21	100.0	7610	9	HUMTRPM2A1
C 19	21	100.0	134514	2	AC025192
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C 21	21	100.0	234431	9	AF311103
C 22	21	100.0	334051	2	AC123374 Rattus no
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C 24	19.4	92.4	181	6	AK093399 Sequence
C 25	19.4	92.4	221	6	AX701616
C 26	17.8	84.8	66565	9	AC092103
C 27	17.8	84.8	136131	9	AC000360
C 28	17.8	84.8	147750	10	AC122503
C 29	17.8	84.8	173513	9	HSJ125H2
C 30	17.8	84.8	180230	10	AC124692
C 31	17.8	84.8	191410	10	AC083814
C 32	17.8	84.8	227330	10	AC020786
C 33	17.8	84.8	288888	9	HSJ10932
C 34	17.4	82.9	177102	9	HSJ1069C8
C 35	17.4	82.9	225376	2	AC094230
C 36	17.4	82.9	226229	2	AC102656
C 37	17.4	82.9	241215	2	AC113683
C 38	17.4	82.9	246769	2	AC094144
C 39	17.4	82.9	262108	2	AC105555
C 40	16.8	80.0	345	9	AY062323
C 41	16.8	80.0	1785	6	AX653539
C 42	16.8	80.0	10029	1	AE011998
C 43	16.8	80.0	60786	2	AC124317
C 44	16.8	80.0	120873	9	AL445986
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ALIGNMENTS

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DEFINITION Sequence 14 from patent US 6541603.
ACCESSION AR302784
VERSION AR302784.1 GI:31691271
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 195)
AUTHORS Kirschling,D.J., Gudkov,A. and Roninson,I.B.
TITLE Genes and genetic elements associated with sensitivity to platinum-based drugs
JOURNAL Patent: US 6541603-A 14 01-APR-2003;

AR302784 195 bp mRNA linear PAT 12-JUN-2003

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  PAT 30-MAR-2001
ACCESSION
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VERSION
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KEYWORDS
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ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
  1
  Xu, J. and Stolk, J.A.
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RESULT 3
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LOCUS
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  PAT 18-SEP-2002
ACCESSION
  BD117323
VERSION
  BD117323.1 GI:23212227
KEYWORDS
  JP 2002010789-A/9400.
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  (Bases 1 to 482)
  Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.
  EST and encoded human protein
  Patent: JP 2002010789-A 9400 15-JAN-2002;
  GENSET CORP
COMMENT
  OS Homo sapiens (human)
  PN JP 2002010789-A/9400
  PD 15-JAN-2002
  PF 07-AUG-2000 JP 2000280989
  PR 05-AUG-1999 US 60/147499
  PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EYE PI
  GIORDANO

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PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
  C12N1/21,
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
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Db 163 ATTGCTGAGACCGCTCTGGTC 143

RESULT 4
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LOCUS
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  Sequence tag and encoded human protein.
  PAT 27-AUG-2002
ACCESSION
  BD027496
VERSION
  BD027496.1 GI:22569238
KEYWORDS
  JP 2001269182-A/3742.
  Homo sapiens (human)
SOURCE
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REFERENCE
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  (Bases 1 to 491)
  Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
  Sequence tag and encoded human protein
  Patent: JP 2001269182-A 3742 02-OCT-2001;
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COMMENT
  OS Homo sapiens (human)
  PN JP 2001269182-A/3742
  PD 02-OCT-2001
  PF 24-FEB-2000 JP 2000118773
  PR 26-FEB-1999 US 60/122487
  PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
  PI JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
  C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68 //G06F17/30, C12N15/00, C12N5/00, PC
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FT CDS 108..161.
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Qy 1 ATTGCTGAGACCGCTCTGGTC 21
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SOURCE		unclassified.		unclassified.		unclassified.		unclassified.		unclassified.			
ORGANISM		unclassified.		unclassified.		unclassified.		unclassified.		unclassified.			
REFERENCE		1 (bases 1 to 512)		JP 2001519667-A/109		JP 2001519667-A/109		JP 2001519667-A/109		JP 2001519667-A/109			
AUTHORS		Jacobs, K., McCoy, J.M., Lavallie, E.R., Racie, L.A., Merberg, D., Treacy, M., Spaulding, V. and Agostino, M.J.		JP 2001519667-A/109		JP 2001519667-A/109		JP 2001519667-A/109		JP 2001519667-A/109			
TITLE		Secreted expressed sequence tags (sESTs)		JP 2001519667-A/109		JP 2001519667-A/109		JP 2001519667-A/109		JP 2001519667-A/109			
JOURNAL		Patent: JP 2001519667-A/109 23-OCT-2001;		JP 2001519667-A/109		JP 2001519667-A/109		JP 2001519667-A/109		JP 2001519667-A/109			
COMMENT		GENETICS INSTITUTE INC		JP 2001519667-A/109		JP 2001519667-A/109		JP 2001519667-A/109		JP 2001519667-A/109			
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PD		23-OCT-2001		JP 1998543069		JP 1998543069		JP 1998543069		JP 1998543069			
PF		10-APR-1998		JP 1998543069		JP 1998543069		JP 1998543069		JP 1998543069			
PR		10-APR-1997		US 08/838821		JP 1998543069		JP 1998543069		JP 1998543069			
PI		KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI		JP 1998543069		JP 1998543069		JP 1998543069		JP 1998543069			
PI		DAVID MERBERG		JP 1998543069		JP 1998543069		JP 1998543069		JP 1998543069			
PI		MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC		JP 1998543069		JP 1998543069		JP 1998543069		JP 1998543069			
C1		N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K38/17 CC		JP 1998543069		JP 1998543069		JP 1998543069		JP 1998543069			
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LOCUS		Sequence 24 from Patent WO02072830.		AX600212		AX600212		AX600212		AX600212			
DEFINITION		AX600212		AX600212		AX600212		AX600212		AX600212			
ACCESSION		AX600212		AX600212		AX600212		AX600212		AX600212			
VERSION		AX600212.1		GI:28400254									
KEYWORDS		Homo sapiens (human)											
SOURCE		Homo sapiens											
ORGANISM		Homo sapiens											
REFERENCE		1											
AUTHORS		Yue, H., Yao, M.G., Ison, C.H., Lu, Y., Warren, B.A., Elliott, V.S., Baughn, M.R., Ding, L., Xu, Y., Gietzen, K.J., Tang, T.Y., Lai, P.G., Duggan, B.M., Burford, N., Lu, D.A., Richardson, T.W., Tran, U.K., Khare, R. and Wallia, N.K.											
TITLE		Proteins associated with cell growth, differentiation, and death											
JOURNAL		Patent: WO 02072830-A 24 19-SEP-2002;											
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Matches		21; Conservative		0; Mismatches		0; Indels		0; Gaps					
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DB		121 ATTGCTGAGACCGTCTGGTC 101											
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LOCUS		Sequence 3 from patent US 6383808.		AR208704		AR208704		AR208704		AR208704			
DEFINITION		AR208704		AR208704		AR208704		AR208704		AR208704			
ACCESSION		AR208704		AR208704		AR208704		AR208704		AR208704			
VERSION		AR208704.1		GI:21509928									
KEYWORDS		Unknown.											
SOURCE		Unknown.											
ORGANISM		Unclassified.											
REFERENCE		1 (bases 1 to 1648)											
AUTHORS		Monia, B.P. and Freier, S.M.											
TITLE		Antisense inhibition of clusterin expression											
JOURNAL		Patent: US 6383808-A 3 07-MAY-2002;											
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DB		139 ATTGCTGAGACCGTCTGGTC 119											
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LOCUS		Human TRPM-2 mRNA, complete cds.		HUMTRPM2A		HUMTRPM2A		HUMTRPM2A		HUMTRPM2A			
DEFINITION		HUMTRPM2A		HUMTRPM2A		HUMTRPM2A		HUMTRPM2A		HUMTRPM2A			
ACCESSION		M64722		M64722		M64722		M64722		M64722			
VERSION		M64722.1		GI:339972									
KEYWORDS		TRPM-2 protein.											
SOURCE		Homo sapiens (human)											
ORGANISM		Homo sapiens											
REFERENCE		1 (sites)											
AUTHORS		Wong, P., Pineault, J., Lakins, J., Taillefer, D., Leger, J., Wang, C. and Tenniswood, M.											
TITLE		Genomic organization and expression of the rat TRPM-2 (clusterin) gene, a gene implicated in apoptosis											
JOURNAL		J. Biol. Chem. 268 (7), 5021-5031 (1993)											
MEDLINE		93186813											
PUBMED		7680346											
REFERENCE		2 (bases 1 to 1648)											
AUTHORS		Wong, P., Taillefer, D., Lakins, J., Pineault, J., Chader, G. and Tenniswood, M.											
TITLE		Molecular characterization of human TRPM-2/clusterin, a gene associated with sperm maturation, apoptosis and neurodegeneration											
JOURNAL		Eur. J. Biochem. 221 (3), 917-925 (1994)											
MEDLINE		94237156											
PUBMED		8181474											
COMMENT		Original											
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DEFINITION	blood plasma component having a biological activity of inhibiting cytolytic mediated by a cytolytic protein.						
ACCESSION	A21577						
VERSION	A21577.1	GI:579601					
KEYWORDS	Homo sapiens (human)						
SOURCE	Homo sapiens						
ORGANISM	Homo sapiens						
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.						
AUTHORS	1 (bases 1 to 1651)						
TITLE	CYTOLYSIS INHIBITOR PROTEINS (CLI) AND DNA SEQUENCES CODING FOR SAID PROTEINS						
JOURNAL	Patent: WO 9105043-A 3 18-APR-1991;						
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 LLENDROTHMLDVMQDFSRASSIIDELFQDFRFTREPQDTYHYLPSLPHRRPHE
 PKSRIVSLMPFSPPELNFHMFQPFLEHQAQQANDIHFSHPAFQHPPTFFIRE
 GDDRTVCREIRHNSGCKRILSDCTNNPSQAKIRELDESQVAE
 RLTRKYNELLSYQWMLNTGSLLEQNEQFNWVSRLANLTQGEDQYLYLVTVASH
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 199..261
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 262..876
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 877..1542
 /product="complement cytolysis inhibitor b-chain"

BASE COUNT 405 a 481 c 447 g 318 t
 ORIGIN Unreported.
 Query Match 100.0%; Score 21; DB 9; Length 1651;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGCTGGTC 21
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 Db 282 ATGTGCTGAGACCGCTGGTC 262

BC019588 1658 bp mRNA linear PRI 17-APR-2003
 Homo sapiens clusterin (complement lysis inhibitor, SP-40, 40,
 sulfated glycoprotein 2, testosterone-repressed prostate message 2,
 apolipoprotein J), mRNA (CDNA clone MGC:24903 IMAGE:4915444),
 complete cds.

ACCESSION BC019588
 VERSION BC019588.1 GI:18043614
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1658)
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zesberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, J., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E.,
 Schnurch, A., Schein, J.E., Jones, S.O. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences

TITLE
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 MEDLINE 22388257
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 1658)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (19-DEC-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk

Email: cgabs-i@mail.nih.gov
 Tissue Procurement: David N. Louis, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 29 Row: m Column: 21
 This clone was selected for full length sequencing because it
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FEATURES
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 /lab_host="DH10B"
 /note="vector: pCMV-SPORT6"
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/product="clusterin (complement lysis inhibitor, SP-40, 40,
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 message 2, apolipoprotein J)"
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 FPKSRIVSLMPFSPPELNFHMFQPFLEHQAQQANDIHFSHPAFQHPPTFFIRE
 EGDDRTVCREIRHNSGCKRILSDCTNNPSQAKIRELDESQVAE
 RLTRKYNELLSYQWMLNTGSLLEQNEQFNWVSRLANLTQGEDQYLYLVTVASH
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 423 a 486 c 439 g 310 t

BASE COUNT 423 a 486 c 439 g 310 t
 ORIGIN
 Query Match 100.0%; Score 21; DB 9; Length 1658;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGCTGGTC 21
 |||||
 Db 135 ATGTGCTGAGACCGCTGGTC 115

RESULT 13
 HSCSP40/C
 LOCUS HSCSP40 1676 bp mRNA linear PRI 22-MAR-1995
 DEFINITION Human SP-40, 40 mRNA for complement-associated protein SP-40, 40
 alpha-1 and beta-1 chain.
 X14723
 ACCESSION X14723.1 GI:30250
 VERSION
 KEYWORDS complement-associated protein; serum protein; SP-40, 40 gene.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1676)

AUTHORS Kirsbaum, L., Sharpe, J.A., Murphy, B., d'Apice, A.J., Classon, B., Hudson, P. and Walker, I.D.

TITLE Molecular cloning and characterization of the novel, human complement-associated protein, SP-40,40: a link between the complement and reproductive systems

JOURNAL EMO J. 8 (3), 711-718 (1989)

MEDLINE 89251601

PUBMED 2721499

REFERENCE 2 (bases 1 to 1676)

AUTHORS Kirsbaum, L.

TITLE Direct Submission

JOURNAL Submitted (17-MAR-1989) Kirsbaum L., The University of Melbourne, The Preclinical Centre, School of Veterinary Science, Parkville Victoria 3052, Australia

COMMENT The sequence overlaps with that reported by Murphy et. al. in J. Clin. Invest. 81:1858-1864(1988).

FEATURES source location/Qualifiers 1..1676 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="LX (107)" /tissue_type="liver" /clone_lib="lambda gt11" 48..1397 /note="SP-40,40 prepropeptide (AA -22 to 427)" /codon_start=1 /protein_id="CAA32847.1" /db_xref="GI:30251" /db_xref="SWISS-PROT:P10909" /translation="MMKLLIFVGLLITWESGVLGQDTVSNLEQMSNQSKYVNEIQNVANGVQIKTLIEKTEERKLLSNLEAKKKEDALNRESETKIKELPGVCNETMALWESCKPCLQTKMFKYARVCRSGSLVGRLEEFLLNQSPFFYFMNGDRIDSLLENDRQTHMLDMVDHPSRASSIIDELFQDRFTFPQDTYHLPFLSPHRRPHFPPKSRIVRSLMPSPYEPFLNHPAMQPFLEMTHEAQAMDIFHSPAPQHPPTBPIR EGGDDRTVCREIRHNSGCLRMKQCDKCREILSVDCSTNPNPQAKLRELEDSLOVAERLTRKNELLKSYQWKLNTSSLLQLNHEQFNWSELNLTQGEQDYILRVITVASHTSQSDVPSGVTEVVVKLFDSDFIVTVFVSVSRKNPKFMTVAEKALQYIRKKHRE" 48..113 /note="signal peptide (AA -22 to -1)" 729..1394 /product="mature alpha-chain (AA 205-427)" 114..1394 /note="SP-40,40 propetide (AA 1-427)" 114..5114 /note="beta-chain" 1622..1627 /note="pot. polyA signal"

BASE COUNT 436 a 488 c 437 g 315 t

ORIGIN

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Db 134 ATTGCTCTGAGACCGTCTGGTC 114

RESULT 14

AX202086/c

LOCUS AX202086

DEFINITION Sequence 16 from Patent WO0153531.

ACCESSION AX202086

VERSION AX202086.1

KEYWORDS GI:15391872

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Phippard, D., Vasanthakamur, G., Dotson, S. and Ma, X.J.

TITLE Osteoarthritis tissue derived nucleic acids, polypeptides, vectors, and cells

JOURNAL Patent: WO 0153531-A 16 26-JUL-2001; Pharmacia Corporation (US)

FEATURES source location/Qualifiers 1..1678 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" 424 a 491 c 450 g 313 t

BASE COUNT

ORIGIN

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Db 156 ATTGCTCTGAGACCGTCTGGTC 136

RESULT 15

BC010514/c

LOCUS BC010514

DEFINITION Homo sapiens clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein U), mRNA (cDNA clone MGC:18080 IMAGE:4150452), complete cds.

ACCESSION BC010514

VERSION BC010514.1

KEYWORDS GI:14714740

SOURCE MGC.

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 1684)

AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.F., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Young, A.C., Shavchenko, Y., Sanchez, A., Whiting, M., Touchman, J.W., Green, E.D., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Bitterfield, S., Krzywinski, M.I., Skalska, U., Smalish, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REFERENCE 2 (bases 1 to 1684)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (10-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-re@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.

CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: angbcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.W., Nanavati,
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 19 Row: 0 Column: 12.

FEATURES

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BASE COUNT 433 a 493 c 448 g 310 t

ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 1684;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGCTGTC 21
 Db 155 ATTGCTGAGACCGCTGTC 135

Search completed: January 21, 2004, 12:11:43
 Job time : 807 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 10:59:47 ; Search time 1733 seconds

(without alignments)
294.515 Million cell updates/sec

Title: US-09-913-325-5

Perfect score: 21

Sequence: 1 attgtctgagaccgtctggtc 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estnu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_estc.*

9: gb_est1.*

10: gb_est2.*

11: gb_est3.*

12: gb_est4.*

13: gb_est5.*

14: gb_est6.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_man.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_pbg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	152	9 AW161759	AW161759 au70a10.x
2	21	100.0	156	10 BF922862	BF922862 OV4-NT024
3	21	100.0	161	10 BF921576	BF921576 MR1-NT017
4	21	100.0	165	10 BF929381	BF929381 IL2-NT019

c	5	21	100.0	167	10	BF929953	IL2-NT019
c	6	21	100.0	169	10	BE766895	RC2-NT011
c	7	21	100.0	177	9	AL048592	DRF2P586H
c	8	21	100.0	177	10	BF958041	RC5-NN116
c	9	21	100.0	184	10	BF958930	PM1-NN120
c	10	21	100.0	185	12	BI036860	MR4-NT014
c	11	21	100.0	190	12	BI037432	CM3-NT026
c	12	21	100.0	193	10	BF944445	RC5-NN116
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c	15	21	100.0	207	10	BF957858	PM1-NN120
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c	17	21	100.0	218	9	AI904991	IL-BT072-
c	18	21	100.0	220	9	BF920102	MR1-NT017
c	19	21	100.0	223	10	AW161224	au70a10.y
c	20	21	100.0	224	9	BF935119	MR4-NT014
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c	22	21	100.0	227	10	BE841947	MR4-STC09
c	23	21	100.0	229	10	BF950916	CM3-NN021
c	24	21	100.0	236	9	AA339299	EST44448
c	25	21	100.0	238	10	BF921875	CM3-NT017
c	26	21	100.0	238	10	BF923639	MR4-NT014
c	27	21	100.0	243	9	AA336628	EST41242
c	28	21	100.0	244	10	BE766870	RC2-NT011
c	29	21	100.0	248	10	BF923643	MR4-NT014
c	30	21	100.0	252	10	BF923633	MR4-NT014
c	31	21	100.0	253	10	BF887875	OV2-TN017
c	32	21	100.0	253	12	BI041998	MR4-NT014
c	33	21	100.0	256	12	BI041248	MR4-NT014
c	34	21	100.0	257	9	AA365743	EST76594
c	35	21	100.0	262	10	BF947155	MR3-NN021
c	36	21	100.0	262	13	BQ339859	PM1-NN120
c	37	21	100.0	266	9	AA352030	EST59959
c	38	21	100.0	268	10	BF920149	MR1-NT017
c	39	21	100.0	272	10	BF956582	PM1-NN120
c	40	21	100.0	273	10	BF956584	PM1-NN120
c	41	21	100.0	274	12	BI036852	MR4-NT014
c	42	21	100.0	277	9	AA351754	EST59817
c	43	21	100.0	280	10	BF935974	IL2-NT019
c	44	21	100.0	283	10	BF947214	MR3-NN021
c	45	21	100.0	284	12	EG95096	CMO-HT129
c		21	100.0	293	9	AA318247	EST20305

ALIGNMENTS

RESULT 1
AW161759

LOCUS

DEFINITION

IMAGE:2781594 3' similar to gb:XI4723 CLUSTERIN PRECURSOR (HUMAN);

mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AW161759 152 bp mRNA linear EST 09-NOV-1999

au70a10.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone

IMAGE:2781594 3' similar to gb:XI4723 CLUSTERIN PRECURSOR (HUMAN);

mRNA sequence.

AW161759 GI:6300792

AW161759.1 Homo sapiens (human)

EST.

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 152)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,

Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin

, J., Moore, B., Scheilenberg, K., Steptoe, M., Tan, F., Theising, B.,

White, Y., Wylie, T., Waterston, R. and Wilson, R.

WashU-NCI human EST Project

Unpublished

Other ESTs: au70a10.y1

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.

FEATURES

Location/Qualifiers
1. .152

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2781594"

/sex="male"

/tissue_type="frontal lobe"

/dev_stage="5 months post-conception"

/lab_host="DH10B"

/clone_lib="Schneider fetal brain 00004"

/note="Organ: brain; vector: pBluescript SK (Stratagene); Site 1: SstI; Site 2: XhoI; Double-stranded cDNA was prepared from human fetal brain tissue. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-GAGAGAGAGAGAGCTCAAGATCCTTAATAATTAATCCCCCCCCCCC-3' and 3' adaptor sequence: 5'-GAGAGAGAGAGCTCGATGTTTCTTTTCTTTT-3'. The library was size-selected for >0.5 kb inserts and has an average insert size estimated at 1.2 kb. This library was constructed using the CAP-trapper method for full-length enrichment and has not undergone amplification. Library was constructed by Dr. Claudio Schneider (LNCIB-Area Science Park, Trieste, Italy)."

27 a 43 c 28 g 54 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 152;
Best Local Similarity 100.0%; Pred. NO. 7.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTGCTGAGACCGCTGGTC 21

Db 100 ATTGCTGAGACCGCTGGTC 120

RESULT 2

BF922862/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Simpson A.J.G.

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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR1&t2=MR1-NT0179-171100-004-g01&t3=2000-11-17&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 16

High quality sequence stop: 161.

Location/Qualifiers

1. .161

/organism="Homo sapiens"

/mol_type="mRNA"

FEATURES

source

(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV4&t2=QV4-NT0247-201100-262-g12&t3=2000-11-20&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 15

High quality sequence stop: 155.

Location/Qualifiers

1. .156

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="NT0247"

/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

38 a 30 c 51 g 37 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 156;

Best Local Similarity 100.0%; Pred. No. 7.2;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTGCTGAGACCGCTGGTC 21

Db 94 ATTGCTGAGACCGCTGGTC 74

RESULT 3

BF921576/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR1&t2=MR1-NT0179-171100-004-g01&t3=2000-11-17&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 16

High quality sequence stop: 161.

Location/Qualifiers

1. .161

/organism="Homo sapiens"

/mol_type="mRNA"

FEATURES

source

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/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NT0179"
/notes="Organ: nervous tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
44 a 29 c 53 g 35 t

BASE COUNT
ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 161;
Best Local Similarity 100.0%; Pred. No. 7.3; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

QY 1 ATTGCTGAGACCGTCTGGTC 21
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DB 101 ATTGCTGAGACCGTCTGGTC 81

RESULT 4
BF929381
LOCUS IL2-NT0198-081200-280-G01 NT0198 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION BF929381
VERSION BF929381.1 GI:12327509
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
MEDLINE
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-NT0198-
081200-280-G01&t3=2000-12-08&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 165.
Location/Qualifiers
1. .165
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NT0198"
/notes="Organ: nervous tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

FEATURES
source

BASE COUNT 44 a 29 c 53 g 35 t
ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 161;
Best Local Similarity 100.0%; Pred. No. 7.3; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

QY 1 ATTGCTGAGACCGTCTGGTC 21
|||||
DB 101 ATTGCTGAGACCGTCTGGTC 81

RESULT 5
BF929953/c
LOCUS IL2-NT0198-111200-293-A03_1 NT0198 Homo sapiens cDNA, mRNA
DEFINITION
ACCESSION BF929953
VERSION BF929953.1 GI:12328185
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
MEDLINE
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COMMENT Contact: Simpson A.J.G.
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-NT0198-
111200-293-A03_1&t3=2000-12-11&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 165.
Location/Qualifiers
1. .167
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NT0198"
/notes="Organ: nervous tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 60 a 32 c 48 g 27 t
ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 167;
Best Local Similarity 100.0%; Pred. No. 7.4; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

QY 1 ATTGCTGAGACCGTCTGGTC 21
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```

Db      54 ATTGCTGAGACCGCTCTGGTC 34

RESULT 6
BE766895/c
LOCUS      BE766895      169 bp      mRNA      linear      EST 19-SEP-2000
DEFINITION RC2-NT0110-050600-013-f03 NT0110 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BE766895
VERSION     BE766895.1 GI:10196819
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 169)
AUTHORS     Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE       Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE     20202663
PUBMED      10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=4&t2=RC2-NT0110-050
            600-013-f03&t3=2000-06-05&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 18
            High quality sequence stop: 169.

FEATURES             source
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    Location/Qualifiers
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="DKFZp586H092"
        /tissue_type="uterus"
        /dev_stage="adult"
        /lab_hosts="DH10B"
        /clone_lib="586 (synonym: hute1)"
        /notes=vector: pspori1, Site_1: NotI, Site_2: SalI/NotI
    BASE COUNT      40 a      41 c      64 g      32 t
    ORIGIN
        Query Match      100.0%; Score 21; DB 9; Length 177;
        Best Local Similarity 100.0%; Pred. No. 7.5;
        Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATTGCTGAGACCGCTCTGGTC 21
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        143 ATTGCTGAGACCGCTCTGGTC 123

Db      143 ATTGCTGAGACCGCTCTGGTC 123

RESULT 8
BF958041/c
LOCUS      BF958041      177 bp      mRNA      linear      EST 22-JAN-2001
DEFINITION RC5-NN1165-281100-033-E03 NN1165 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BF958041
VERSION     BF958041.1 GI:12375316
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 177)
AUTHORS     Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE       Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE     20202663
PUBMED      10737800

Db      125 ATTGCTGAGACCGCTCTGGTC 105

RESULT 7
AL048592/c
LOCUS      AL048592      177 bp      mRNA      linear      EST 01-MAR-2000
DEFINITION DKFZp586H092_r1 586 (synonym: hute1) Homo sapiens cDNA clone
ACCESSION  AL048592
            DKFZp586H092, mRNA sequence.

QY      1 ATTGCTGAGACCGCTCTGGTC 21
        |||||
        125 ATTGCTGAGACCGCTCTGGTC 105

Db      125 ATTGCTGAGACCGCTCTGGTC 105

RESULT 7
AL048592/c
LOCUS      AL048592      177 bp      mRNA      linear      EST 01-MAR-2000
DEFINITION DKFZp586H092_r1 586 (synonym: hute1) Homo sapiens cDNA clone
ACCESSION  AL048592
            DKFZp586H092, mRNA sequence.

```

COMMENT Contact: Simpson A.J.G.
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-NN1165-281100-033-B03&t3=2000-11-28&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 177.

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN1165"
/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
47 a 34 c 52 g 28 t

BASE COUNT
63 a 34 c 52 g 28 t

ORIGIN
Query Match 100.0%; Score 21; DB 10; Length 177;
Best Local Similarity 100.0%; Pred. No. 7.5; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0;

QY 1 ATTGCTCGAGACCGTCGTGTC 21
|||||

Db 68 ATTGCTCGAGACCGTCGTGTC 48
|||||

RESULT 9
BF958930/c
LOCUS BF958930 184 bp mRNA linear EST 22-JAN-2001
DEFINITION PM1-NN1200-011200-009-g08 NN1200 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF958930
VERSION BF958930.1 GI:12376205
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 184)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
PUBMED
COMMENT Contact: Simpson A.J.G.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-NN1165-281100-033-B03&t3=2000-11-28&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 177.

FEATURES
source
1..184
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN1200"
/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
47 a 36 c 61 g 40 t

BASE COUNT
47 a 36 c 61 g 40 t

ORIGIN
Query Match 100.0%; Score 21; DB 10; Length 184;
Best Local Similarity 100.0%; Pred. No. 7.6; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0;

QY 1 ATTGCTCGAGACCGTCGTGTC 21
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Db 108 ATTGCTCGAGACCGTCGTGTC 88
|||||

RESULT 10
BI036860/c
LOCUS BI036860 185 bp mRNA linear EST 14-JUN-2001
DEFINITION MR4-NT0140-080101-209-c09 NT0140 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI036860
VERSION BI036860.1 GI:14443486
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 185)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
PUBMED
COMMENT Contact: Simpson A.J.G.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-NT0140-080101-209-c09&t3=2001-01-08&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 134.

FEATURES
source
1..185
/organism="Homo sapiens"
/mol_type="mRNA"

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/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NT0140"
/notes="Organ: nervous tumor; Vector: puc18; Site: 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      41 a  42 c  62 g  40 t
ORIGIN
Query Match      100.0%; Score 21; DB 12; Length 185;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGCTCTGGTC 21
|||||
Db 109 ATTGCTGAGACCGCTCTGGTC 89
|||||

RESULT 11
BI037432/c
LOCUS          190 bp      mRNA      linear      EST 14-JUN-2001
DEFINITION    CM3-NT0267-110101-588-h12 NT0267 Homo sapiens cDNA, mRNA sequence.
ACCESSION     BI037432
VERSION       BI037432.1 GI:14444058
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 190)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
PUBMED
Contact: Simpson A.J.G.
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-NT0267-
110101-588-h12&t3=2001-01-11&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 4
High quality sequence stop: 190.
Location/Qualifiers
1..190
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NT0267"
/notes="Organ: nervous tumor; Vector: puc18; Site: 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      70 a  39 c  57 g  27 t
ORIGIN
Query Match      100.0%; Score 21; DB 10; Length 193;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGCTCTGGTC 21
|||||

```

```

BASE COUNT      76 a  38 c  49 g  27 t
ORIGIN
Query Match      100.0%; Score 21; DB 12; Length 190;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGCTCTGGTC 21
|||||
Db 36 ATTGCTGAGACCGCTCTGGTC 16
|||||

RESULT 12
BF944445/c
LOCUS          193 bp      mRNA      linear      EST 22-JAN-2001
DEFINITION    RC5-NN1165-131000-021-D04 NN1165 Homo sapiens cDNA, mRNA sequence.
ACCESSION     BF944445
VERSION       BF944445.1 GI:12361720
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 193)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
PUBMED
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-NN1165-
131000-021-D04&t3=2000-10-13&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 193.
Location/Qualifiers
1..193
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN1165"
/notes="Organ: nervous normal; Vector: puc18; Site: 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      70 a  39 c  57 g  27 t
ORIGIN
Query Match      100.0%; Score 21; DB 10; Length 193;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGCTCTGGTC 21
|||||

```

Db 72 ATTGCTGAGACCGCTGTGGTC 52

RESULT 13
 A1745406 196 bp mRNA linear EST 17-DEC-1999
 LOCUS wc37d01.x1 NCI CGAP P228 Homo sapiens cDNA clone IMAGE:2320801 3'
 DEFINITION similar to gb:K14723 CLUSTERIN PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION A1745406
 VERSION A1745406.1 GI:5113694
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 196)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished
 CONTACT: Robert Straubeberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone Distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.lnl.gov/bbrp/image/image.html
 Insert Length: 264 Std Error: 0.00
 Seq primer: -40UP from Gibco.

FEATURES
 Location/Qualifiers
 1..196
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2320801"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH103"
 /clone_lib="NCI-CGAP P228"
 /note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)
 with a modified polylinker; Plasmid DNA from the
 normalized library NCI CGAP P222 was prepared, and as
 circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clones IDs
 985608-986759, 120192-120195, and 1217928-1220615).
 Subtraction by Bento Soares and M. Fatima Bonaldo."
 39 a 60 c 35 g 62 t

BASE COUNT
 ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 196;
 Best Local Similarity 100.0%; Pred. No. 7.8;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGCTGTGGTC 21
 |||||
 Db 101 ATTGCTGAGACCGCTGTGGTC 121
 |||||

RESULT 14
 BF957666/c 201 bp mRNA linear EST 22-JAN-2001
 LOCUS FMI-NN1200-251100-007-c09 NN1200 Homo sapiens cDNA, mRNA sequence.
 DEFINITION
 ACCESSION BF957666
 VERSION BF957666.1 GI:12374941
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 201)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM1&t2=PM1-NN1200-
 251100-007-c09&t3=2000-11-25&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 14
 High quality sequence stop: 201.

FEATURES
 Location/Qualifiers
 1..201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="NN1200"
 /note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 52 a 59 c 71 g 39 t

BASE COUNT
 ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 201;
 Best Local Similarity 100.0%; Pred. No. 7.9;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGCTGTGGTC 21
 |||||
 Db 125 ATTGCTGAGACCGCTGTGGTC 105
 |||||

RESULT 15
 BF957858/c 207 bp mRNA linear EST 22-JAN-2001
 LOCUS FMI-NN1200-271100-008-a07 NN1200 Homo sapiens cDNA, mRNA sequence.
 DEFINITION
 ACCESSION BF957858
 VERSION BF957858.1 GI:12375133
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 207)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1&t2=PM1-NN1200-271100-008-a07&t3=2000-11-27&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence start: 24
 High quality sequence stop: 182.

FEATURES
 source
 1..207
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="NN1200"
 /note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 BASE COUNT 51 a 45 c 71 g 40 t
 ORIGIN
 Query Match 100.0%; Score 21; DB 10; Length 207;
 Best Local Similarity 100.0%; Pred. No. 8;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATTGCTGAGACCGCTGTGTC 21
 |||||
 Db 143 ATTGCTGAGACCGCTGTGTC 123

Search completed: January 21, 2004, 13:09:41
 Job time : 1738 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 10:04:17 ; Search time 148 Seconds
(without alignments)
383.028 Million cell updates/sec

Title: US-09-913-325-5

Perfect score: 21
Sequence: 1 attgtctgagaccgtctggtc 21

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 252756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
25: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	AAA94227	Human testosterone
C 2	21	100.0	195	AAT00416	Genetic suppressor
C 3	21	100.0	396	AAF94824	Human ovarian carc
C 4	21	100.0	396	ABT03091	Human ovarian carc
C 5	21	100.0	396	ABL48774	Ovarian carcinoma
C 6	21	100.0	491	AAC03751	Human secreted pro
C 7	21	100.0	512	AAV89150	EST clone CG1. Ho
C 8	21	100.0	572	AAZ42136	Human normal bladd

ALIGNMENTS

RESULT 1

AAA94227
ID AAA94227 standard; DNA; 21 BP.
XX AAA94227;
AC AAA94227;
XX 12-JAN-2001 (first entry)
XX Human testosterone-repressed prostate message-2 antisense oligo #3.
DE Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;
KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX Homo sapiens.
XX WO200049937-A2.
XX 31-AUG-2000.
XX 25-FEB-2000; 2000WO-US04875.
XX 26-FEB-1999; 99US-0121726.
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX Gleave M, Rennie PS, Miyake H, Nelson C;
XX WPI; 2000-533132/48.
XX Treating prostatic tumors and renal cancers by antisense inhibition of
PT the testosterone-repressed prostate messenger-2 gene -

Human ovarian anti
Human secreted exp
Toxicologically re
cDNA encoding nove
Human cDNA encodin
Human clusterin ge
Cytolysis inhibito
Human clusterin ge
Osteoarthritis tis
Human cDNA encodin
Human clusterin ge
Human G protein-co
Human secreted pro
Human secreted pro
Human secreted pro
Human secreted pro
Human secreted pro
Human structural p
Arabidopsis thalia
cDNA encoding nove
Human Oestrogen re
Bifidobacterium lo
Bifidobacterium lo
Human immune/haema
Human colon cancer
DNA encoding novel
Human reproductive
Nucleotide sequenc
EP-892847 Seq ID 4
DNA encoding CARDI
Drosophila melanog
Drosophila melanog
Drosophila melanog
Drosophila melanog
Drosophila melanog
Human cDNA differs
Human DNA contain

XX Claim 4; Page 36; 38pp; English.
 XX
 XX The present sequence is an antisense oligonucleotide directed at the
 CC human testosterone-repressed prostate message-2 (TRPM-2), also known as
 CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
 CC promote the regression of tumours, and oligonucleotides directed
 CC at human TRPM-2 can be used in the treatment of tumour cells expressing
 CC the TRPM-2 gene. These include prostate cancer, renal cell cancer and
 CC some breast cancer cells. In addition to this, they also increase the
 CC chemosensitivity of the cells, meaning that conventional chemotherapy is
 CC more effective.
 XX
 SQ Sequence 21 BP; 3 A; 5 C; 6 G; 7 T; 0 other;

Query Match 100.0%; Score 21; DB 21; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.25; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATTGCTGAGACCGCTCTGGTC 21
 Db 1 ATTGCTGAGACCGCTCTGGTC 21

RESULT 2
 AAT00416/c
 ID AAT00416 standard; cDNA; 195 BP.
 XX
 AC AAT00416;
 DT 26-MAR-1996 (first entry)
 DE Genetic suppressor element HL7.1.
 XX
 XX Genetic suppressor element; GSE; platinum-based drug; cisplatin;
 KW chemotherapy; HL7.1; testosterone-repressed prostatic message-2; TRPM-2;
 KW ss.
 XX
 OS Synthetic.
 XX
 XX WO9522612-A2.
 XX
 XX 24-AUG-1995.
 XX
 XX 22-FEB-1995; 95WO-US02303.
 XX
 XX 22-FEB-1994; 94US-0199900.
 XX
 XX (UNII) UNIV ILLINOIS FOUND.
 XX
 XX Gudkov A, Kirschling DJ, Robinson IB;
 XX WPI; 1995-302718/39.
 XX
 XX Genetic suppressor elements which confer resistance to
 PT platinum-based drugs, eg. cisplatin, on cancer cells - useful for
 PT enhancement of chemotherapy, and for diagnosis of resistance to
 PT these drugs.
 XX
 PS Claim 14; Fig 17; 75pp; English.

XX The sequences represented by AAT00405-T00418 are genetic suppressor
 CC elements (GSEs). This sequence represents GSE HL6.10. This sequence
 CC shows homology to the cDNA encoding testosterone-repressed prostatic
 CC message-2 (TRPM-2). These sequences were obtained from a cDNA library
 CC derived from the total cDNA of a cisplatin sensitive cell. Genetic
 CC suppressor elements confer resistance to platinum-based drugs (PDs),
 CC such as cisplatin. These functional GSEs can then be used to create
 CC probes for the parent gene. The probes can then be used in a method of
 CC measuring the level of GSE gene expression. The GSEs can be used in
 CC methods of diagnosis of resistance to PDs by measuring the level of
 CC expression of GSE genes. The GSEs are also used in methods to overcome
 CC resistance to PDs in cancer cells. The GSEs (or fragments of them) can

CC be used to inhibit the function of genes associated with sensitivity to
 CC PDs. For enhancement of chemotherapy, a GSE can be transferred (either
 CC alone or with another gene) on an expression vector into blood to
 CC progenitor cells from a cancer patient. The cells are returned to the
 CC patients circulation and allowed to repopulate the blood before
 CC aggressive chemotherapy is carried out (using higher cisplatin
 CC concentrations than normal), this will thereby avoid toxic side effects
 CC to the immune system as the blood cells will be GSE resistant.
 XX
 SQ Sequence 195 BP; 46 A; 45 C; 71 G; 33 T; 0 other;

Query Match 100.0%; Score 21; DB 16; Length 195;
 Best Local Similarity 100.0%; Pred. No. 0.37;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATTGCTGAGACCGCTCTGGTC 21
 Db 153 ATTGCTGAGACCGCTCTGGTC 133

RESULT 3
 AAF94824/c
 ID AAF94824 standard; cDNA; 396 BP.
 XX
 AC AAF94824;
 DT 23-MAY-2001 (first entry)
 DE Human ovarian cancer associated coding sequence SEQ ID NO: 15.
 XX
 KW Human, ovarian cancer; vaccine; gene therapy; carcinoma; ss.
 OS Homo sapiens.
 XX
 XX WO200118046-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 08-SEP-2000; 2000WO-US24827.
 XX
 PR 10-SEP-1999; 99US-0394374.
 PR 01-MAY-2000; 2000US-0561778.
 PR 15-AUG-2000; 2000US-0640173.
 PR 07-SEP-2000; 2000US-0656668.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Stolk JA;
 XX
 DR WPI; 2001-211395/21.

XX Isolated polypeptides associated with ovarian carcinomas, and the
 PT nucleic acids that encode them, useful for the prevention diagnosis and
 PT treatment of ovarian cancers -
 XX
 PS Claim 18; Page 120; 189pp; English.
 XX
 XX The present invention provides a number of coding sequences and proteins,
 CC the over-expression of which is associated with ovarian carcinoma/cancer.
 CC These can be used in the diagnosis, treatment and prevention of ovarian
 CC cancer, optionally by gene therapy or in the form of a vaccine. The
 CC present sequence is an example of one of these sequences.
 XX
 SQ Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 1 other;

Query Match 100.0%; Score 21; DB 22; Length 396;
 Best Local Similarity 100.0%; Pred. No. 0.42;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATTGCTGAGACCGCTCTGGTC 21
 Db 145 ATTGCTGAGACCGCTCTGGTC 125

XX 03-APR-2001; 2001US-0825294.
 XX
 XX 10-SEP-1999; 99US-0394374.
 PR 01-MAY-2000; 2000US-0561778.
 PR 15-AUG-2000; 2000US-0640173.
 PR 07-SEP-2000; 2000US-0656668.
 PR 14-NOV-2000; 2000US-0713550.
 XX
 XX (XUJ/) XU J.
 PA (STOL/) STOLK J A.
 PA (ALGA/) ALGATE P A.
 XX (FLIN/) FLING S P.
 XX
 XX Xu J, Stolk JA, Algate PA, Fling SP;
 XX WPI; 2002-171027/22.
 XX
 XX Ovarian tumour polypeptide and polynucleotide useful in diagnosis, -
 PT prevention and/or treatment of cancer, especially ovarian cancer
 XX
 XX Example 1; Page 43; 131pp; English.
 XX
 XX The invention relates to ovarian tumour polynucleotides and polypeptides
 CC that may be utilised in cancer therapy, for example in a vaccine or
 CC gene therapy. Polypeptides and polynucleotides of the invention are
 CC useful for detecting a cancer in a patient, for stimulating and/or
 CC expanding T-cells specific for a tumour protein, and for inhibiting the
 CC development of a cancer in a patient. They are also useful for
 CC stimulating an immune response in a patient, and for treating a cancer in
 CC a patient and for determining the presence of a cancer in a patient.
 CC The isolated polynucleotides of the invention are useful for their
 CC ability to selectively form duplex molecules with complementary stretches
 CC of the entire desired gene or gene fragments, and for designing and
 CC preparing ribozyme molecules for inhibiting expression of tumour
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
 CC invention are also useful in recombinant DNA molecules to direct
 CC expression of a polypeptide in appropriate host cells. The sequences
 CC given in records ABL48760-ABL48956 represent polynucleotides encoding
 CC ovarian carcinoma proteins.
 XX
 XX Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 1 other;
 SQ
 Query Match 100.0%; Score 21; DB 24; Length 396;
 Best Local Similarity 100.0%; Pred. No. 0.42;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 QY 1 ATTGCTCAGACCGCTCGTC 21
 Db 145 ATTGCTCAGACCGCTCGTC 125
 RESULT 6
 AAC03751/c
 ID AAC03751 standard; cDNA; 491 BP.
 XX AAC03751;
 AC
 DT 06-OCT-2000 (first entry)
 XX
 DE Human secreted protein 5' EST, SEQ ID NO: 3749.
 XX
 XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss.
 XX
 XX Homo sapiens.
 OS
 XX EF1033401-A2.
 PN
 XX 06-SEP-2000.
 PD
 XX 21-FEB-2000; 2000EP-0200610.
 PP
 XX

PR 26-FEB-1999; 99US-0122487.
 XX (GBST) GENSET.
 XX Dumas Milne Edwards J, Duclert A, Giordano J;
 XX WPI; 2000-500381/45.
 DR P-PSDB; AAG03745.
 XX
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX
 XX Claim 1; SEQ ID 3749; 71pp + CD-ROM; English.
 XX
 XX The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. An ORF has been identified within the
 CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
 CC derived from 30 different tissues. EST sequences usually correspond
 CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
 CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
 CC well suited for isolating cDNA sequences derived from the 5' ends of
 CC mRNAs and even in those cases where longer cDNA sequences have been
 CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
 CC mRNAs with intact 5' ends and can therefore be used to obtain full length
 CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
 CC gene therapy and chromosome mapping procedures. They are used to obtain
 CC upstream regulatory sequences and to design expression and secretion
 CC vectors.
 XX
 XX SQ Sequence 491 BP; 149 A; 114 C; 149 G; 78 T; 1 other;
 Query Match 100.0%; Score 21; DB 21; Length 491;
 Best Local Similarity 100.0%; Pred. No. 0.43;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATTGCTGAGACCGTCTGGTC 21
 DB 194 ATTGCTGAGACCGTCTGGTC 174
 RESULT 7
 AAV89150/c
 ID AAV89150 standard; cDNA; 512 BP.
 AC AAV89150;
 XX
 DT 15-FEB-1999 (first entry)
 XX EST clone CGL.
 DE Human; secreted protein; expressed sequence tag; EST; haematopoiesis;
 KW tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic;
 KW receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
 KW gene therapy; ss.
 XX Homo sapiens.
 OS
 XX WO9845436-A2.
 PN
 XX 15-OCT-1998.
 PD
 XX 10-APR-1998; 98WO-US06955.
 PF
 XX 10-APR-1997; 97US-0838821.
 PR (GEMY) GENETICS INST INC.
 XX Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
 PI Racie LA, Spaulding V, Treacy M;
 XX WPI; 1999-070077/06.
 DR
 XX

PT New polynucleotides encoding human secreted proteins - derived from
 PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,
 PT ovary, pituitary, retina and colon cDNA libraries.
 XX Claim 1; Page 126; 618pp; English.
 XX
 XX The present sequence represents a human expressed sequence tag (EST).
 CC The polynucleotide, which is a secreted EST, and the encoded protein
 CC are predicted to have useful biological activities which would make
 CC them suitable for treating, preventing or ameliorating medical
 CC conditions in humans and animals, although no supporting data is
 CC given. Suggested activities include nutritional activity, immune
 CC stimulating or suppressing activity, haematopoiesis regulating
 CC chemotactic/chemokinetic activity, haemostatic and thrombolytic
 CC activity, receptor/ligand activity, anti-inflammatory activity,
 CC cadherin/tumour invasion suppressor activity, tumour inhibition
 CC activity. The polynucleotide may also be useful for gene therapy.
 XX
 XX SQ Sequence 512 BP; 154 A; 114 C; 150 G; 94 T; 0 other;
 Query Match 100.0%; Score 21; DB 20; Length 512;
 Best Local Similarity 100.0%; Pred. No. 0.43;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATTGCTGAGACCGTCTGGTC 21
 DB 121 ATTGCTGAGACCGTCTGGTC 101
 RESULT 8
 AAZ42136/c
 ID AAZ42136 standard; cDNA; 572 BP.
 XX
 AC AAZ42136;
 XX
 DT 31-JAN-2000 (first entry)
 XX Human normal bladder tissue cDNA derived EST 15.
 DE Human; bladder; treatment; EST; expressed sequence tag; cytostatic;
 XX cancer; gene therapy; ss.
 KW Homo sapiens.
 OS
 XX DE19818620-A1.
 PN
 XX 28-OCT-1999.
 PD
 XX 21-APR-1998; 98DE-1018620.
 PF
 XX 21-APR-1998; 98DE-1018620.
 PR (META-) METAGEN GES GENOMFORSCHUNG MBH.
 PA Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
 XX WPI; 1999-602416/52.
 DR
 XX New polypeptides and their nucleic acids, useful for treatment of
 PT bladder tumour and identification of therapeutic agents -
 PT
 XX Claim 3; Page 158; 366pp; German.
 XX
 XX This invention describes novel polypeptide fragment sequences (I) and
 CC their encoding nucleic acids (II) which are highly expressed in normal
 CC bladder tissue and have cytostatic activity. (II) are used for
 CC recombinant expression of (I) and to isolate complete genes. (I) are
 CC used to identify agents suitable for the treatment of bladder tumours,
 CC to directly treat this form of cancer (including expression from gene
 CC therapy vectors), or are used in a preparation for cancer treatment. (I)
 CC is also used for the generation of specific antibodies. (II) are
 CC identified by assembling ESTs (expressed sequence tags) from a

particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, and therefore reduces the number of failures because of ESTs from different libraries representing different parts of the same unknown gene. CC
 CC distorting the estimated frequency of occurrence in a particular tissue. CC
 CC AA24122-24248 represent EST fragments derived from a human normal CC
 CC bladder tissue cDNA library which encode the protein fragments CC
 CC represented in AA240329-Y60591. CC
 CC
 CC Sequence 572 BP; 161 A; 128 C; 186 G; 97 T; 0 other; CC
 CC
 CC Query Match 100.0%; Score 21; DB 20; Length 572; CC
 CC Best Local Similarity 100.0%; Pred. No. 0.44; 0; Indels 0; Gaps 0; CC
 CC Matches 21; Conservative 0; Mismatches 0; CC
 CC
 CC QY 1 ATTGCTGAGACCGTCTGGTC 21 CC
 CC ||||| CC
 CC Db 262 ATTGCTGAGACCGTCTGGTC 242 CC
 CC
 CC RESULT 9 CC
 CC ABQ56105/c CC
 CC ID ABQ56105 standard; cDNA; 704 BP. CC
 CC AC ABQ56105; CC
 CC XX CC
 CC DT 22-AUG-2002 (first entry) CC
 CC XX CC
 CC DE Human ovarian antigen HSPSH41 cDNA, SEQ ID NO:1985. CC
 CC XX CC
 CC KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; CC
 CC KW ovarian cancer; breast cancer; tumour; reproductive system disorder; CC
 CC KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; CC
 CC KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; CC
 CC KW inflammatory condition; immune disorder; blood disorder; CC
 CC KW cardiovascular disorder; respiratory disorder; neurological disorder; CC
 CC KW gastrointestinal disorder; urinary system disorder; drug screening; CC
 CC KW gene therapy; chromosome mapping; forensic analysis; CC
 CC KW antibody preparation; cytostatic; immunomodulatory; neuroprotective; CC
 CC KW antiinflammatory; gynaecological; reproductive; gene; ss. CC
 CC XX CC
 CC OS Homo sapiens. CC
 CC XX CC
 CC PN WO200200677-A1. CC
 CC XX CC
 CC PD 03-JAN-2002. CC
 CC XX CC
 CC PF 07-JUN-2001; 2001WO-US18569. CC
 CC XX CC
 CC PR 07-JUN-2000; 2000US-209467P. CC
 CC XX CC
 CC PA (HUMA-) HUMAN GENOME SCI INC. CC
 CC XX CC
 CC PI Birse CE, Rosen CA; CC
 CC XX CC
 CC DR WPI; 2002-147878/19. CC
 CC DR P-PSDB; ABP43028. CC
 CC XX CC
 CC PT Isolated nucleic acid molecules encoding novel ovarian polypeptides, CC
 CC PT useful in the prevention treatment and diagnosis of cancer (e.g. CC
 CC PT ovarian cancer), immune disorders, cardiovascular disorders and CC
 CC PT neurological diseases - CC
 CC XX CC
 CC PS Claim 1; SEQ ID NO 1985; 2922pp; English. CC
 CC XX CC
 CC CC The invention relates to 2175 novel human ovarian antigens (ABP41054- CC
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also CC
 CC CC encompasses polypeptides 90% identical and polynucleotides 95% identical CC
 CC to the sequences of the invention. The invention additionally relates to CC
 CC recombinant vectors and host cells comprising human ovarian antigen CC
 CC polynucleotides, antibodies against human ovarian antigens, and the use CC
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing, CC
 CC CC treating, prognosing or preventing various ovary and/or breast-related

disorders. Such conditions include ovarian cancer and breast cancer, and CC
 CC metastatic tumours of ovarian or breast origin, reproductive system CC
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation, CC
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine CC
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic CC
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and CC
 CC vaginitis), immune disorders (e.g., congenital and acquired CC
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), CC
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders, CC
 CC respiratory disorders, neurological disorders, gastrointestinal disorders CC
 CC and urinary system disorders. Ovarian antigen polypeptides and CC
 CC polynucleotides may also be used in screening for compounds which CC
 CC modulate ovarian antigen expression or activity. The polynucleotides may CC
 CC further be used for gene therapy, chromosome mapping, in the CC
 CC identification of individuals and in forensic analysis, and the CC
 CC polypeptides may be used as food additives or to prepare antibodies CC
 CC useful in disease diagnosis, drug targeting and phenotyping. The present CC
 CC sequence represents cDNA encoding a human ovarian antigen of the CC
 CC invention. CC
 CC Note: The sequence data for this patent did not form part of the printed CC
 CC specification, but was obtained in electronic format directly from WIPO CC
 CC at ftp.wipo.int/pub/published_pct_sequences. CC

Sequence 704 BP; 180 A; 197 C; 199 G; 121 T; 7 other; CC
 CC
 CC Query Match 100.0%; Score 21; DB 24; Length 704; CC
 CC Best Local Similarity 100.0%; Pred. No. 0.46; CC
 CC Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0; CC

QY 1 ATTGCTGAGACCGTCTGGTC 21

Db 215 ATTGCTGAGACCGTCTGGTC 195

RESULT 10

AAA43857/c

ID AAA43857 standard; cDNA; 922 BP.

XX AAA43857;

XX

DT 21-AUG-2000 (first entry)

XX

DE Human secreted expressed sequence tag SEQ ID NO:432.

XX Human; mouse; chicken; rat; secreted expressed sequence tag; sEST; CC
 CC expressed sequence tag; EST; probe; chemotactic; proliferative; CC
 CC immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic; CC
 CC thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal; CC
 CC antiviral; antidiabetic; antiasthmatic; vulnary; antiparkinsonian; CC
 CC anticancer; osteoprotective; neuroprotective; nootropic; antipsoriatic; CC
 CC cerebroprotective; anticonvulsant; antidepressant; gene therapy; CC
 CC vaccine; autoimmune disorder; multiple sclerosis; allergic condition; CC
 CC insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; CC
 CC lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; CC
 CC central nervous system disorder; Alzheimer's disease; stroke; CC
 CC Parkinson's disease; Huntington's disease; coagulation disorder; CC
 CC haemophilia; thrombosis; inflammatory disorder; Crohn's disease; CC
 CC tumour; infection; depression; psoriasis; ss. CC

XX Homo sapiens.

OS

PN WO2000021991-A1.

XX

PD 20-APR-2000.

XX

PF 15-OCT-1999; 99WO-US24206.

XX

PR 15-OCT-1998; 98US-0104436.

XX

PA (GENY) GENETICS INST INC.

XX

PI Jacobs K, McCoy JM, laVallie ER, Collins-Racie LA, Evans C;

PI Merberg D, Treacy M, Bowman MR;

XX WPI; 2000-317938/27.
 XX Isolated polynucleotides, and encoded proteins, comprising secreted
 PT expressed sequence tags (ESTs), useful for treating various disorders
 PT such as autoimmune, infectious, and central nervous system disorders -
 XX
 PS Claim 1; Page 316; 803pp; English.
 XX
 CC AAA43426 to AAA45925 represent specifically claimed secreted expressed
 CC sequence tags (ESTs), isolated from human, mouse, chicken and rat
 CC tissue sources. The ESTs can have a range of activities depending on
 CC the tissues they were isolated from. The activities include:
 CC chemotactic; proliferative; immunomodulatory; haematopoietic;
 CC chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;
 CC cytosstatic; antibacterial; antifungal; antiviral; antidiabetic;
 CC antiasthmatic; vulnerary; antitumor; osteopathic; neuroprotective;
 CC neurotropic; antiparkinsonian; antipsoriatic; cerebroprotective;
 CC anticonvulsant; and antidepressant. The ESTs can be used for gene
 CC therapy and in vaccines. The ESTs are useful as probes for the
 CC identification and isolation of full-length cDNAs and genomic DNA
 CC molecules which correspond to the ESTs. Proteins encoded by the ESTs
 CC are useful in assays for determining biological activity and raising
 CC antibodies. They may be useful for treatment of autoimmune disorders
 CC - (multiple sclerosis, insulin dependent diabetes), allergic conditions
 CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
 CC osteoporosis, osteoarthritis, central nervous system disorders
 CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
 CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
 CC disease), tumours, bacterial, fungal or viral infections, depression and
 CC psoriasis. AAA45926 to AAA45931 represent linker variants which are given
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 922 BP; 243 A; 265 C; 244 G; 166 T; 4 other;
 Query Match 100.0%; Score 21; DB 21; Length 922;
 Best Local Similarity 100.0%; Pred. No. 0.48;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATTGTCGAGACCGTCGTGTC 21
 |||||
 DB 118 ATTGTCGAGACCGTCGTGTC 98
 |||||
 RESULT 11
 ABZ83527/c
 ID ABZ83527 standard; cDNA; 1024 BP.
 XX
 AC ABZ83527;
 XX
 DT 14-MAY-2003 (first entry)
 XX
 DE Toxicologically relevant human nucleotide sequence #686.
 XX
 KW Toxicologically relevant gene; toxicological response; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0203016500-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 16-AUG-2002; 2002WO-US26514.
 XX
 PR 16-AUG-2001; 2001US-313080P.
 XX
 PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
 XX
 PI Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schweizer K;
 PI Allen P;
 XX
 DR WPI; 2003-268322/26.
 XX

PT Determining a toxicological response to an agent, useful for screening
 PT of drugs, comprises comparing the expression profile of one or more
 PT human toxic response genes to a reference gene expression profile
 PT indicative of toxicity -
 XX
 PS Claim 1; Page 232; 455pp; English.
 XX
 CC The present invention describes a method (M1) for determining a
 CC toxicological response to an agent, which comprises comparing the
 CC expression profile of one or more human toxic response genes to a
 CC reference gene expression profile indicative of toxicity, and so
 CC determining the presence of a toxic response to the agent. Also
 CC described: (1) an array comprising one or more polynucleotides selected
 CC from the genes corresponding to the partial sequences given in AB282842
 CC to AB284764, or their fragments of at least 20 nucleotides, or
 CC homologues; and (2) determining if a gene putatively identified to be a
 CC toxic response gene plays a role on toxic response pathways by
 CC determining the expression profile of the gene after exposure of cells
 CC or a human subject to a known toxic pharmaceutical or industrial agent,
 CC comprising: (a) exposing cells to an agent; (b) obtaining the test gene
 CC expression profile for a putatively identified toxic response gene after
 CC exposure to a known toxic pharmaceutical or industrial agent; and
 CC (c) comparing the test profile to the expression profile of a gene with
 CC a similar function or comparing the test profile to the expression
 CC profile of that gene after exposure to other known toxic compounds. The
 CC methods are useful for predicting and determining toxicological responses
 CC on a cellular, organ or system level. The arrays comprising the human
 CC genes are useful for toxicological screening of drugs, pharmaceutical
 CC compounds and chemicals.
 XX
 SQ Sequence 1024 BP; 262 A; 299 C; 278 G; 185 T; 0 other;
 Query Match 100.0%; Score 21; DB 25; Length 1024;
 Best Local Similarity 100.0%; Pred. No. 0.49;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATTGTCGAGACCGTCGTGTC 21
 |||||
 DB 134 ATTGTCGAGACCGTCGTGTC 114
 |||||
 RESULT 12
 AAS44948/c
 ID AAS44948 standard; cDNA; 1568 BP.
 XX
 AC AAS44948;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE cDNA encoding novel human secretory protein, Seq ID No 29.
 XX
 KW Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KW fertility; analgesic; pain; antigen; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200166689-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 05-MAR-2001; 2001WO-US04942.
 XX
 PR 07-MAR-2000; 2000US-0519705.
 PR 19-MAY-2000; 2000US-0574454.
 PR 17-JUN-2000; 2000US-0596193.
 PR

PR 14-JUL-2000; 2000US-0616847.
 PR 19-SEP-2000; 2000US-0665363.
 PR 20-OCT-2000; 2000US-0693267.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren P, Ma Y, Zhou P;
 PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AD, Wang J;
 PI WPI; 2001-589934/56.
 DR P-PSDB; AAU28048.
 XX Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders -
 XX
 XX Claim 1; SEQ ID No 29; 107bp; English.
 XX The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC analgesic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAS44920-AAS45295 represent novel human secreted protein
 CC coding sequences of the invention.
 XX
 XX Sequence 1568 BP; 386 A; 456 C; 434 G; 292 T; 0 other;
 XX
 XX Query Match 100.0%; Score 21; DB 22; Length 1568;
 XX Best Local Similarity 100.0%; Pred. No. 0.52;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 ATTGTCGACACCGTCTGGTC 21
 DB 156 ATTGTCGACACCGTCTGGTC 136
 XX
 RESULT 13
 ABS78654/c
 ID ABS78654 standard; cDNA; 1589 BP.
 XX
 AC ABS78654;
 XX
 XX 16-DEC-2002 (first entry)
 DT
 XX Human cDNA encoding CGDD12, INCYTE 7503618CB1.
 DE
 XX

Human; ss; gene; cell growth; differentiation; death; CGDD; cancer;
 KW cell proliferative disorder; arteriosclerosis; atherosclerosis;
 KW cirrhosis; hepatitis; paroxysmal nocturnal haemoglobinuria; psoriasis;
 KW polycythaemia vera; primary thrombocytopaenia; developmental disorder;
 KW renal tubular acidosis; anaemia; mental retardation; epilepsy; AIDS;
 KW neurological disorder; Alzheimer disease; Parkinson's disease; asthma;
 KW reproductive disorder; infertility; autoimmune disorder; gout; allergy;
 KW inflammatory disorder; acquired immunodeficiency syndrome; uveitis;
 KW autoimmune thyroiditis; contact dermatitis; Crohn's disease; infection;
 KW diabetes mellitus; glomerulonephritis; irritable bowel syndrome;
 KW multiple sclerosis; osteoarthritis; osteoporosis; pancreatitis;
 KW rheumatoid arthritis.

Homo sapiens.

WO200272830-A2.

19-SEP-2002.

08-FEB-2002; 2002WO-US03715.

09-FEB-2001; 2001US-268111P.

23-FEB-2001; 2001US-271175P.

08-MAR-2001; 2001US-274503P.

09-MAR-2001; 2001US-274552P.

(INCY-) INCYTE GENOMICS INC.

Yue H, Yao MG, Ison CH, Lu Y, Warren BA, Elliott VS, Baughn MR;
 Ding L, Xu Y, Gietzen KJ, Tang TY, Lal PG, Duggan BM, Burford N;
 Lu DAM, Richardson TW, Tran UK, Khare R, Walla NK;

WPI; 2002-723356/78.

P-PSDB; ABG97361.

New human proteins associated with cell growth, differentiation and
 death, useful for diagnosing, treating or preventing autoimmune or
 inflammatory disorders (e.g. AIDS, allergy or anaemia), cancer,
 atherosclerosis or hepatitis

Claim 5; Page 180-181; 181pp; English.

The invention relates to an isolated polypeptide comprising CGDD1-12
 (cell growth, differentiation and death), a naturally occurring amino
 acid sequence at least 90% identical to CGDD, a biologically active
 fragment or an immunogenic fragment. Also included are the
 polynucleotides encoding CGDD1-12, a recombinant polynucleotide
 comprising a promoter sequence operably linked to the CGDD
 polynucleotides, a cell transformed with the recombinant polynucleotide,
 a transgenic organism comprising the recombinant polynucleotide, an
 anti-CGDD antibody, screening for compounds which bind to/modulate
 or are ant/agonists of CGDD or alter the expression of CGDD
 polynucleotide and a CGDD polynucleotide microarray.
 The polypeptides, polynucleotides, agonists and antagonists are
 useful for diagnosing, treating or preventing disorders associated with
 aberrant expression of CGDD, particularly cell proliferative (e.g.
 arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal
 nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary
 thrombocytopaenia or cancer), developmental disorders (e.g. renal
 tubular acidosis, anaemia or mental retardation), neurological disorders
 (e.g. Alzheimer disease, Parkinson's disease or epilepsy),
 reproductive disorders (e.g. infertility or a disruption in the
 menstrual cycle), or autoimmune/inflammatory disorders (e.g. AIDS,
 acquired immunodeficiency syndrome) allergies, asthma, autoimmune
 thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus,
 glomerulonephritis, gout, irritable bowel syndrome, multiple sclerosis,
 osteoarthritis, osteoporosis, pancreatitis, rheumatoid arthritis,
 uveitis, or viral, bacterial, fungal, parasitic, protozoal or helminthic
 infections. They are also useful in the assessment of the effects of
 exogenous compounds on the expression of nucleic acid and amino acid
 sequences of proteins associated with CGDD. The present sequence
 encodes a CGDD protein.

XX

SQ Sequence 1589 BP; 407 A; 421 C; 466 G; 295 T; 0 other;
 Query Match 100.0%; Score 21; DB 24; Length 1589;
 Best Local Similarity 100.0%; Pred. No. 0.53;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATTGCTGTGAGACCGCTGTGGTC 21
 |||||
 Db 164 ATTGCTGTGAGACCGCTGTGGTC 144

RESULT 14
 ABN99656/c
 ID ABN99656 standard; DNA; 1648 BP.
 XX
 AC ABN99656;
 XX
 DT 16-AUG-2002 (first entry)
 XX
 DE Human clusterin gene sequence 1.
 XX
 KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
 KW hypercholesterolaemia; cardiovascular disorder; ds;
 KW hyperproliferative disorder; hyperlipidemic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200222635-A1.
 XX
 PD 21-MAR-2002.
 XX
 PF 10-SEP-2001; 2001WO-US28235.
 XX
 PR 11-SEP-2000; 2000US-0659791.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Freier SM;
 XX
 DR WPI; 2002-404805/43.
 DR P-PSDB; AAO15039.
 XX
 PT Novel antisense compound targeted to nucleic acid molecule encoding
 PT clusterin, useful for treating animal having disease associated with
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder -
 XX
 PS Example 13; Page 89-92; 125pp; English.
 XX
 CC The invention comprises antisense oligonucleotides that are capable of
 CC inhibiting expression of the human clusterin gene. The antisense
 CC oligonucleotides of the invention are useful for inhibiting the
 CC expression of clusterin in cells. The antisense oligonucleotides are also
 CC useful for treating an animal with a disease or condition associated with
 CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present
 CC DNA sequence represents a human clusterin gene sequence.
 XX
 SQ Sequence 1648 BP; 408 A; 488 C; 440 G; 312 T; 0 other;
 Query Match 100.0%; Score 21; DB 24; Length 1648;
 Best Local Similarity 100.0%; Pred. No. 0.53;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATTGCTGTGAGACCGCTGTGGTC 21
 |||||
 Db 139 ATTGCTGTGAGACCGCTGTGGTC 119

RESULT 15
 AAO11503/c
 ID AAO11503 standard; DNA; 1651 BP.
 XX
 AC AAO11503;

XX 20-JUN-1991 (first entry)
 DT Cytolysis Inhibitor gene.
 DE Cytolysis inhibitor; perforin; immunological effector molecule;
 XX infertility; ss.
 KW Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT sig_peptide 199..261
 FT /*tag= a
 FT mat_peptide 262..1542
 FT /*tag= b
 FT /product= cytolysis inhibitor
 XX
 PN DE3933850-A.
 XX
 PD 18-APR-1991.
 XX
 PF 06-OCT-1989; 89DE-3933850.
 XX
 PR 06-OCT-1989; 89DE-3933850.
 XX
 PA (SCHD) SCHERING AG.
 XX
 PI Tschopp J, Jenne D;
 XX
 DR WPI; 1991-118338/17.
 XX
 PT DNA sequence coding for cytolysis inhibitor - is strong inhibitor
 PT of terminal complement protein, e.g. perforin secreted by killer
 PT cells
 XX
 PS Claim 2; Page 8; 15pp; German.
 XX
 CC Two probes were prepared based on the known partial amino acid
 CC sequences of both chains of the Cytolysis Inhibitor and used to
 CC screen a liver-specific cDNA library. One clone which hybridised
 CC positively to both probes was found to contain a 1.7Kb BamHI-XbaI
 CC fragment. This was inserted into plasmid pGEM4, to give pGEM4/Zi-1.
 CC E.coli transformed with the plasmid are deposited under DSM # 5269.
 CC The insert has the sequence given in this file.
 CC See also AAO11501 and AAO11502.
 XX
 SQ Sequence 1651 BP; 405 A; 481 C; 447 G; 318 T; 0 other;
 Query Match 100.0%; Score 21; DB 12; Length 1651;
 Best Local Similarity 100.0%; Pred. No. 0.53;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATTGCTGTGAGACCGCTGTGGTC 21
 |||||
 Db 282 ATTGCTGTGAGACCGCTGTGGTC 262

Search completed: January 21, 2004, 11:44:45
 Job time : 151 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 12:11:53 ; Search time 217 Seconds
(without alignments)

341.106 Million cell updates/sec

Title: US-09-913-325-5

Perfect score: 21 attgtctgagaccgtctgtgc 21

Sequence: 1 attgtctgagaccgtctgtgc 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2324096 seqs, 1762381658 residues

Total number of hits satisfying chosen parameters: 4649192

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/prodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/prodata/2/pubpna/US05_NEW_PUB.seq:*
- 4: /cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/prodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/prodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/prodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/prodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*
- 14: /cgn2_6/prodata/2/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/prodata/2/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*
- 17: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	10	US-09-944-326-5
2	21	100.0	21	13	US-09-967-726A-5
3	21	100.0	21	13	US-10-080-794-5
	21	100.0	21	12	US-10-404-579-14
C 4	21	100.0	396	9	US-09-825-294-15
C 5	21	100.0	396	10	US-09-970-965-15
C 6	21	100.0	396	12	US-10-369-186-15
C 7	21	100.0	396	13	US-10-361-811-15
C 8	21	100.0	396	16	US-10-212-677-15
C 9	21	100.0	461	11	US-09-918-995-32172
C 10	21	100.0	462	11	US-09-918-995-2524
C 11	21	100.0	465	11	US-09-918-995-32177
C 12	21	100.0	492	11	US-09-918-995-31156
C 13	21	100.0	532	10	US-09-833-381-910
C 14	21	100.0	532	10	US-09-833-381-910
C 15	21	100.0	539	11	US-09-918-995-31688

C 16	21	100.0	704	12	US-10-264-049-1985
C 17	21	100.0	1451	13	US-10-133-013-214
C 18	21	100.0	1568	12	US-10-291-172-29
C 19	21	100.0	1614	13	US-10-119-428-31
C 20	21	100.0	1678	10	US-09-765-231A-16
C 21	21	100.0	1775	13	US-10-133-013-243
C 22	21	100.0	2090	13	US-09-814-353-20893
C 23	19.4	92.4	181	12	US-10-404-579-19
C 24	19.4	92.4	490	11	US-09-918-995-12511
C 25	19.4	92.4	491	11	US-09-918-995-17455
C 26	18.4	87.6	277	10	US-09-833-381-1241
C 27	17.8	84.8	1670	11	US-09-832-129-30
C 28	17.8	84.8	1684	11	US-09-832-129-11
C 29	17.4	82.9	516	11	US-09-918-995-31131
C 30	16.8	80.0	387	15	US-10-156-761-7326
C 31	16.8	80.0	9025608	15	US-10-156-761-1
C 32	16.2	77.1	1728	10	US-09-938-842A-1616
C 33	16.2	77.1	2304	12	US-10-291-172-405
C 34	16.2	77.1	2462	12	US-10-104-047-255
C 35	15.8	75.2	355	15	US-10-106-698-1758
C 36	15.8	75.2	559	13	US-10-029-386-1057
C 37	15.8	75.2	755	15	US-10-013-315-47
C 38	15.8	75.2	1228	11	US-09-919-039-24
C 39	15.8	75.2	1580	11	US-09-764-891-9304
C 40	15.8	75.2	2652	12	US-10-104-047-807
C 41	15.8	75.2	8888	9	US-09-836-077-41
C 42	15.8	75.2	43412	12	US-10-085-117-7
C 43	15.4	73.3	374	12	US-10-428-681-53
C 44	15.2	72.4	25	15	US-10-098-263B-102072
C 45	15.2	72.4	332	11	US-09-764-891-1943

ALIGNMENTS

RESULT 1

US-09-944-326-5
; Sequence 5, Application US/09944326
; Patent No. US20020128220A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
; FILE REFERENCE: UBC P-020-2
; CURRENT APPLICATION NUMBER: US/09/944,326
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-09-944-326-5

Query Match 100.0%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGCTGTGTC 21

DB 1 ATTGCTGAGACCGCTGTGTC 21

RESULT 2

US-09-967-726A-5

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; Sequence 5, Application US/09967726A
; Publication No. US20030159130A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Zellweger, Tobias
; TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2
; FILE REFERENCE: UBC.P-022
; CURRENT APPLICATION NUMBER: US/09/967,726A
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-09-967-726A-5

Query Match          100.0%; Score 21; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTGCTGAGACCGCTGGTC 21
Db 1 ATTGCTGAGACCGCTGGTC 21

RESULT 3
US-10-080-794-5
; Sequence 5, Application US/10080794
; Publication No. US20030166591A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE
; FILE REFERENCE: UBC.P-020-3
; CURRENT APPLICATION NUMBER: US/10/080,794
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/944,326
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-10-080-794-5

Query Match          100.0%; Score 21; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTGCTGAGACCGCTGGTC 21
Db 1 ATTGCTGAGACCGCTGGTC 21

RESULT 4
US-10-404-579-14/c
; Sequence 14, Application US/10404579
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; Publication No. US20040002099A1
; GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J
; APPLICANT: Gudkov, Andrei
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/404,579
; FILING DATE: 01-Apr-2003
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,657A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20040002099A1nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-404-579-14

Query Match          100.0%; Score 21; DB 12; Length 195;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTGCTGAGACCGCTGGTC 21
Db 153 ATTGCTGAGACCGCTGGTC 133

RESULT 5
US-09-825-294-15/c
; Sequence 15, Application US/09825294
; Patent No. US2002000491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 396
; TYPE: DNA
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-15

Query Match      100.0%; Score 21; DB 9; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGTCTGGTC 21
   |||||
Db 145 ATTGCTGAGACCGTCTGGTC 125

RESULT 6
US-09-970-966-15/c
; Sequence 15, Application US/09970966
; Patent No. US2002017363A1
; GENERAL INFORMATION:
; APPLICANT: Moleah, David Alan
; APPLICANT: Stolk, John A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C6
; CURRENT APPLICATION NUMBER: US/09/970,966
; CURRENT FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 333
; OTHER INFORMATION: n = A,T,C or G
US-09-970-966-15

Query Match      100.0%; Score 21; DB 10; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGTCTGGTC 21
   |||||
Db 145 ATTGCTGAGACCGTCTGGTC 125

RESULT 7
US-10-369-186-15/c
; Sequence 15, Application US/10369186
; Publication No. US20030232056A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C9
; CURRENT APPLICATION NUMBER: US/10/369,186
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 333
; OTHER INFORMATION: n = A,T,C or G
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US-10-369-186-15

Query Match      100.0%; Score 21; DB 12; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGTCTGGTC 21
   |||||
Db 145 ATTGCTGAGACCGTCTGGTC 125

RESULT 8
US-10-361-811-15/c
; Sequence 15, Application US/10361811
; Publication No. US20030206918A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C8
; CURRENT APPLICATION NUMBER: US/10/361,811
; CURRENT FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 333
; OTHER INFORMATION: n = A,T,C or G
US-10-361-811-15

Query Match      100.0%; Score 21; DB 13; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGTCTGGTC 21
   |||||
Db 145 ATTGCTGAGACCGTCTGGTC 125

RESULT 9
US-10-212-677-15/c
; Sequence 15, Application US/10212677
; Publication No. US20030129192A1
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 333
; OTHER INFORMATION: n = A,T,C or G
US-10-212-677-15

Query Match      100.0%; Score 21; DB 16; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.58;
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGCTGGTC 21
 |||||
 Db 145 ATTGCTGAGACCGCTGGTC 125

RESULT 10

US-09-918-995-32172/c
 ; Sequence 32172, Application US/09918995
 ; Publication No. US20030073623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FROM VARIOUS CDNA LIBRARIES
 ; FILE REFERENCE: 20411-756
 ; CURRENT APPLICATION NUMBER: US/09/918,995
 ; CURRENT FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: US/09/235,076
 ; PRIOR FILING DATE: 1999-01-20
 ; NUMBER OF SEQ ID NOS: 38054
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 32172
 ; LENGTH: 461
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)...(461)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-918-995-32172

Query Match 100.0%; Score 21; DB 11; Length 461;
 Best Local Similarity 100.0%; Pred. No. 0.58;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGCTGGTC 21
 |||||
 Db 196 ATTGCTGAGACCGCTGGTC 176

RESULT 11

US-09-918-995-2524/c
 ; Sequence 2524, Application US/09918995
 ; Publication No. US20030073623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FROM VARIOUS CDNA LIBRARIES
 ; FILE REFERENCE: 20411-756
 ; CURRENT APPLICATION NUMBER: US/09/918,995
 ; CURRENT FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: US/09/235,076
 ; PRIOR FILING DATE: 1999-01-20
 ; NUMBER OF SEQ ID NOS: 38054
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2524
 ; LENGTH: 462
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)...(462)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-918-995-2524

Query Match 100.0%; Score 21; DB 11; Length 462;
 Best Local Similarity 100.0%; Pred. No. 0.58;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGCTGGTC 21
 |||||
 Db 181 ATTGCTGAGACCGCTGGTC 161

RESULT 12

US-09-918-995-32177/c
 ; Sequence 32177, Application US/09918995
 ; Publication No. US20030073623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FROM VARIOUS CDNA LIBRARIES
 ; FILE REFERENCE: 20411-756
 ; CURRENT APPLICATION NUMBER: US/09/918,995
 ; CURRENT FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: US/09/235,076
 ; PRIOR FILING DATE: 1999-01-20
 ; NUMBER OF SEQ ID NOS: 38054
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 32177
 ; LENGTH: 465
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)...(465)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-918-995-32177

Query Match 100.0%; Score 21; DB 11; Length 465;
 Best Local Similarity 100.0%; Pred. No. 0.58;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGCTGGTC 21
 |||||
 Db 188 ATTGCTGAGACCGCTGGTC 168

RESULT 13

US-09-918-995-31156/c
 ; Sequence 31156, Application US/09918995
 ; Publication No. US20030073623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FROM VARIOUS CDNA LIBRARIES
 ; FILE REFERENCE: 20411-756
 ; CURRENT APPLICATION NUMBER: US/09/918,995
 ; CURRENT FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: US/09/235,076
 ; PRIOR FILING DATE: 1999-01-20
 ; NUMBER OF SEQ ID NOS: 38054
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 31156
 ; LENGTH: 492
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)...(492)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-918-995-31156

Query Match 100.0%; Score 21; DB 11; Length 492;
 Best Local Similarity 100.0%; Pred. No. 0.58;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCGCTGGTC 21
 |||||
 Db 174 ATTGCTGAGACCGCTGGTC 154

RESULT 14

US-09-833-381-910/c
 ; Sequence 910, Application US/09833381

; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 910
; LENGTH: 532
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(532)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-910

Query Match 100.0%; Score 21; DB 10; Length 532;
Best Local Similarity 100.0%; Pred. No. 0.58; 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTCTCTGAGACCGCTGTGGTC 21
|||||
DB 159 ATTCTCTGAGACCGCTGTGGTC 139

RESULT 15

US-09-918-995-31688/C
; Sequence 31688, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31688
; LENGTH: 539
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(539)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31688

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DB 207 ATTCTCTGAGACCGCTGTGGTC 187

Search completed: January 21, 2004, 15:35:43
Job time : 224 secs

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JOURNAL Patent: WO 9954353-A 29 28-OCT-1999;
SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
(DE); PILARSKY CHRISTIAN (DE)

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DEFINITION Sequence 1318 from patent US 6500938.
ACCESSION AR270755
VERSION AR270755.1 GI:29701989
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 1416)
AUTHORS Au-Young, J. and Seilhamer, J.J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1318 31-DEC-2002;
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1. .1416
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BASE COUNT 344 a 440 c 365 g 267 t

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Db 1309 GCTGGCGGAGTTGGGGCCT 1289

RESULT 3
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LOCUS 1416 bp mRNA linear PRI 09-JAN-1995
DEFINITION Human sulfated glycoprotein-2 mRNA, 3' end.
ACCESSION M74816
VERSION M74816.1 GI:338056
KEYWORDS secreted protein; sulfated glycoprotein-2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1416)
AUTHORS Danik, M., Chabot, J.-G., Mercier, C., Benabid, A.L., Chauvin, C.,
Quirion, R. and Suh, M.
TITLE Human gliomas and epileptic foci express high levels of a mRNA
related to rat testicular sulfated glycoprotein 2, a purported
marker of cell death
JOURNAL proc. Natl. Acad. Sci. U.S.A. 88 (19), 8577-8581 (1991)
MEDLINE 92020896
PUBMED 1924317

COMMENT Original source text: Homo sapiens male 63 yr. old adult brain
tumor cDNA to mRNA.

FEATURES
Location/Qualifiers

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LFEKYNELLKSYQWKMLNTSLLEOLNEQPNVSRILANTQGEDOYVLEVTVAHST
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BASE COUNT 344 a 440 c 365 g 267 t

ORIGIN

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Db 1309 GCTGGCGGAGTTGGGGCCT 1289

RESULT 4
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LOCUS 1512 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 59 from Patent WO0175177.
ACCESSION AX302541
VERSION AX302541.1 GI:17383080
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Morin, P.J., Sherman-Baust, C.A., Pizer, E.S. and Hough, C.D.
TITLE Tumor markers in ovarian cancer
JOURNAL Patent: WO 0175177-A 59 11-OCT-2001;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)

FEATURES
source
1. .1512
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BASE COUNT 378 a 461 c 387 g 286 t

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Query Match 100.0%; Score 21; DB 6; Length 1512;
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
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Db 1405 GCTGGCGGAGTTGGGGCCT 1385

RESULT 5
HUMAPOJ/c
LOCUS 1512 bp mRNA linear PRI 31-OCT-1994


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DEFINITION Human apolipoprotein J mRNA, complete cds.
ACCESSION J02908
VERSION J02908.1 GI:1178854
KEYWORDS apolipoprotein J; High density lipoprotein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1512)
AUTHORS de Silva,H.V., Harmony,J.A., Stuart,W.D., Gil,C.M. and Robbins,J.
TITLE Apolipoprotein J: structure and tissue distribution
JOURNAL Biochemistry 29 (22), 5380-5389 (1990)
MEDLINE 90344779
PUBMED 1974459
COMMENT Original source text: Human fetal liver, cDNA to mRNA, clone
lambda[1-3].
Draft entry and computer-readable sequence for [1] kindly submitted
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378 a 461 c 387 g 286 t
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1405 GCTGGCGGAGTTGGGGCCT 1385

RESULT 6
AK093399/c
LOCUS AK093399
DEFINITION Homo sapiens cDNA FLJ36080 fis, clone TEST12019872, highly similar
to CLUSTERIN PRECURSOR.
ACCESSION AK093399
VERSION AK093399.1 GI:21752259
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1512)
AUTHORS Nishi,T., Ota,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K.,
Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,
Sugano,S., Nagahara,K., Masuho,Y., Nagai,K. and Isogai,T.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
MEDLINE 2 (bases 1 to 1546)
PUBMED Isogai,T. and Yamamoto,J.
COMMENT Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomesh@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7
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LOCUS AK093399
DEFINITION Sequence 3 from patent US 6383808.
ACCESSION AK093399
VERSION AK093399.1 GI:21509928
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1648)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 3 07-MAY-2002;
MEDLINE Location/Qualifiers
PUBMED 1..1648
SOURCE source
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/organism="unknown"
408 a 488 c 440 g 312 t
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Best Local Similarity 100.0%; Pred. No. 45;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1541 GCTGGCGGAGTTGGGGCCT 1521

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through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 29 Row: m Column: 21
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/note="Vector: pCMV-SPORT6"
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 misc_feature 1622. .1627
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 LOCUS AX202086 1678 bp DNA linear PAT 30-AUG-2001
 DEFINITION Sequence 16 from Patent WO0153531.
 ACCESSION AX202086
 VERSION AX202086.1 GI:15391872
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Phippard,D., Vasanthakumari,G., Dotson,S. and Ma,X.J.
 TITLE Osteoarthritis tissue derived nucleic acids, polypeptides, vectors,
 and cells
 JOURNAL Patent: WO 0153531-A 16 26-JUL-2001;
 Pharmacia Corporation. (US)
 FEATURES
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 RESULT 10514/c
 LOCUS BC010514 1684 bp mRNA linear PRI 17-APR-2003
 DEFINITION Homo sapiens clusterin (complement lysis inhibitor, SP-40,40,
 sulfated glycoprotein 2, testosterone-repressed prostate message 2,
 apolipoprotein J), mRNA (cDNA clone MGC:18080 IMAGE:4150452),
 complete cds.
 ACCESSION BC010514
 VERSION BC010514.1 GI:14714740
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1684)
Strausberg, R.L., Beigold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, P.S., Wagner, L., Stennan, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalitus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2388257
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2 (bases 1 to 1684)
Strausberg, R.
Direct Submission
Submitted (10-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-x@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louis, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 19 Row: 0 Column: 12.

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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1684)
Strausberg, R.L., Beigold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, P.S., Wagner, L., Stennan, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalitus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2388257
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2 (bases 1 to 1684)
Strausberg, R.
Direct Submission
Submitted (10-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-x@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louis, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 19 Row: 0 Column: 12.

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sulfated glycoprotein 2, testosterone-repressed prostate
message 2, apolipoprotein J)"

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Query Match 100.0%; Score 21; DB 9; Length 1684;
Best Local Similarity 100.0%; Pred. No. 45;
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Db 1555 GCTGGCGGAGTTGGGGCCT 1535
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LOCUS AX330207 3196 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 716 from Patent WO0194629.
ACCESSION AX330207
VERSION AX330207.1 GI:18103185
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
gene sets
Patent: WO 0194629-A 716 13-DEC-2001;
Avalon Pharmaceuticals (US)
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ORIGIN
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QY 1 GCTGGCGGAGTTGGGGCCT 21
Db 2891 GCTGGCGGAGTTGGGGCCT 2871
RESULT 14
AX337122/c
LOCUS AX337122 3196 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 7631 from Patent WO0194629.
ACCESSION AX337122
VERSION AX337122.1 GI:18127841
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature

gene sets
 Patent: WO 0194629-A 7631 13-DEC-2001;
 Avalon Pharmaceuticals (US)
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 Db 2891 GCTGGCGGAGTTGGGGCCT 2871
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 LOCUS Human TRPM-2 protein gene, exons 7,8,9 and complete cds.
 DEFINITION Human TRPM-2 protein gene, exons 7,8,9 and complete cds.
 ACCESSION M63379
 VERSION M63379.1 GI:292841
 KEYWORDS TRPM-2 protein.
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (sites)
 Wong, P., Pineault, J., Lakins, J., Taillefer, D., Leger, J., Wang, C.
 and Tenniswood, M.
 Genomic organization and expression of the rat TRPM-2 (clusterin)
 gene, a gene implicated in apoptosis
 J. Biol. Chem. 268 (7), 5021-5031 (1993)
 93186813
 7680346
 2 (bases 1 to 3196)
 Wong, P., Taillefer, D., Lakins, J., Pineault, J., Chader, G. and
 Tenniswood, M.
 Molecular characterization of human TRPM-2/clusterin, a gene
 associated with sperm maturation, apoptosis and neurodegeneration
 Eur. J. Biochem. 221 (3), 917-925 (1994)
 REFERENCE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 JOURNAL
 MEDLINE
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 /number=7
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 /gene="TRPM-2"
 /number=8
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 /gene="TRPM-2"
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 /gene="TRPM-2"
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 ORIGIN

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 Db 2891 GCTGGCGGAGTTGGGGCCT 2871
 |||||

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 Job time : 805 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 10:04:17 ; Search time 148 Seconds
(without alignments)
383.028 Million cell updates/sec

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Perfect score: 21
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

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Post-processing: Minimum Match 0%
Maximum Match 100%
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 - 23: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA2001B.DAT.*
 - 24: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA2002.DAT.*
 - 25: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	AAA94234	Human testosterone
2	21	100.0	21	AAZ41353	Human normal uteru
3	21	100.0	1416	ACA56720	Human signalling p
4	21	100.0	1512	ASA83111	Apolipoprotein J o
5	21	100.0	1648	ABN98656	Human clusterin ge
6	21	100.0	1678	AAH23086	Osteoarthritis tis
7	21	100.0	2876	AAAC90467	Human uncoupling p
8	21	100.0	3196	ABL62379	Colon adenocarcino

C 9	21	100.0	3196	24	ABL62924	Prostate cancer re
C 10	21	100.0	8133	24	ABN99663	Human clusterin ge
C 11	17.8	84.8	250	24	ABL80072	Human ovarian canc
C 12	17.4	82.9	3845	24	ABQ94233	FL011 gene expres
C 13	17.4	82.9	3732	24	ABQ94271	Fungal gene expres
C 14	16.8	80.0	2137	25	ABZ57220	Human zinc finger
C 15	16.8	80.0	2535	22	AAH25134	Nucleotide sequenc
C 16	16.8	80.0	2535	24	ABX15715	Human 21612 alcoho
C 17	16.8	80.0	2962	20	AAK28161	Rat Acid sensitive
C 18	16.8	80.0	3562	19	AAV60839	Rat acid sensing i
C 19	16.8	80.0	3562	21	AAZ61197	cDNA encoding a ra
C 20	16.8	80.0	3647	19	AAV60842	Rat acid sensing i
C 21	16.8	80.0	3647	21	AAZ61200	cDNA encoding a ra
C 22	16.8	80.0	4121	21	AAZ61317	Human ORFX ORF872
C 23	16.8	80.0	4196	25	ABX711009	Novel human cDNA s
C 24	16.8	80.0	4342	25	ABX08824	Angiogenesis-assoc
C 25	16.8	80.0	4344	25	AAZ53171	Human kinases and
C 26	16.8	80.0	14854	22	AAZ28620	Genomic sequence #
C 27	16.8	80.0	349980	24	ABQ81849	Biifidobacterium lo
C 28	16.4	78.1	50	15	AAQ69840	Simian virus 40 T/
C 29	16.4	78.1	50	18	AAZ64302	SV40 T/t late (ata
C 30	16.4	78.1	50	20	ABX17590	Test sequence from
C 31	16.4	78.1	50	24	ABK83081	DNA binding molecu
C 32	16.4	78.1	58	20	AAV64746	HIV anti-viral oli
C 33	16.4	78.1	68	22	AAH24758	Nucleotide sequenc
C 34	16.4	78.1	144	25	ABZ79849	Simian virus 40 ea
C 35	16.4	78.1	185	10	AAZ90660	Sequence of SV40 e
C 36	16.4	78.1	204	21	AAA12021	Murine lactate deh
C 37	16.4	78.1	223	21	AAA12017	Human enolase A pr
C 38	16.4	78.1	226	24	ABU53832	SV40 promoter. Rh
C 39	16.4	78.1	226	24	ABU53845	SV40 promoter sequ
C 40	16.4	78.1	231	21	AAA12001	Murine PGK HRE der
C 41	16.4	78.1	237	21	AAA12001	Promoter OBHrel us
C 42	16.4	78.1	242	20	AAZ07789	Murine PGK HRE der
C 43	16.4	78.1	242	21	AAA12016	Murine PGK HRE der
C 44	16.4	78.1	243	20	AAZ11397	Murine PGK fragmen
C 45	16.4	78.1	243	21	AAA11995	Murine PGK HRE der

ALIGNMENTS

RESULT 1

- AAA94234
- ID AAA94234 standard; DNA; 21 BP.
- XX AAA94234;
- AC AAA94234;
- XX AAA94234;
- DT 12-JAN-2001 (first entry)
- XX Human testosterone-repressed prostate message-2 antisense oligo #10.
- DE Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;
- XX Human; testosterone-repressed prostate message-2; SGP-2; cancer; antisense oligonucleotide; ss.
- KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
- XX Homo sapiens.
- OS Homo sapiens.
- XX WO200049937-A2.
- PN WO200049937-A2.
- XX 31-AUG-2000.
- PD 31-AUG-2000.
- XX 25-FEB-2000; 2000WO-US04875.
- PF 25-FEB-2000; 2000WO-US04875.
- XX 26-FEB-1999; 99US-0121726.
- PR 26-FEB-1999; 99US-0121726.
- XX (UTBR-) UNIV BRITISH COLUMBIA.

PA Gleave M, Rennie PS, Miyake H, Nelson C;
PI WPI; 2000-533132/48.
DR WPI; 2000-533132/48.
XX Treating prostatic tumors and renal cancers by antisense inhibition of
PT the testosterone-repressed prostate messenger-2 gene -

XX PS Example 5; Page 38; 38pp; English.

XX CC The present sequence is an antisense oligonucleotide directed at the
XX CC human testosterone-repressed prostate message-2 (TRPM-2, also known as
XX CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
XX CC promote the regression of tumours, and oligonucleotides directed
XX CC at human TRPM-2 can be used in the treatment of tumour cells expressing
XX CC the TRPM-2 gene. These include prostate cancer, renal cell cancer and
XX CC some breast cancer cells. In addition to this, they also increase the
XX CC chemosensitivity of the cells, meaning that conventional chemotherapy is
XX CC more effective.

XX SQ Sequence 21 BP; 1 A; 4 C; 12 G; 4 T; 0 other;

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Best Local Similarity 100.0%; Pred. NO. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GCTGGGGGAGTTGGGGGCT 21

RESULT 2

AAZ41353/c
ID AAZ41353 standard; cDNA; 975 BP.

XX AC AAZ41353;

XX DT 19-JAN-2000 (first entry)

XX DE Human normal uterus tissue derived cDNA 29.

XX KW Human; uterus; cancer; treatment; anticancer; cytostatic; gene therapy;
XX KW EST; expressed sequence tag; ss.

XX OS Homo sapiens.

XX PN DE19817946-A1.

XX PD 21-OCT-1999.

XX PF 17-APR-1998; 98DE-1017946.

XX PR 17-APR-1998; 98DE-1017946.

XX PA (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl B;

XX WPI; 1999-591956/51.

XX PT New nucleic acid sequences expressed in normal uterine tissues, and
XX PT derived polypeptides, for treatment of uterine cancer and
XX PT identification of therapeutic agents -

XX PS Claim 3; Page 95; 154pp; German.

XX CC This invention describes novel cDNA sequences (A) highly expressed in
XX CC normal uterine tissue which can have anticancer and cytostatic activity
XX CC and can be used for gene therapy. (A) are used (i) for recombinant
XX CC expression of polypeptides (B) and (ii) to isolate complete genes.
XX CC (B) are used (i) to identify agents suitable for treatment of uterine
XX CC cancer; (ii) directly for treating this form of cancer (including
XX CC expression from gene therapy vectors) and (iii) for generation of
XX CC specific antibodies. (A) are identified by assembling ESTs (expressed
XX CC sequence tags) from a particular tissue type before comparison of the
XX CC expression patterns. This allows a significantly longer fragment of the
XX CC gene to be revealed, so should reduce the number of failures associated
XX CC with the fact that ESTs from different libraries may represent
XX CC different parts of the same unknown gene, distorting the estimated
XX CC frequency of occurrence in a particular tissue. AAZ41325-241385

CC represent the human uterine tissue derived cDNA fragments of the
CC invention which encode the protein fragments represented in
CC CC AAY59838-Y59892.

XX SQ Sequence 975 BP; 221 A; 320 C; 248 G; 186 T; 0 other;

Query Match 100.0%; Score 21; DB 20; Length 975;
Best Local Similarity 100.0%; Pred. NO. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q/ 1 GCTGGGGGAGTTGGGGGCT 21

Db 903 GCTGGGGGAGTTGGGGGCT 883

RESULT 3

ACA56720/c

ID ACA56720 standard; cDNA; 1416 BP.

XX AC ACA56720;

XX DT 06-JUN-2003 (first entry)

XX DE Human signalling pathway polynucleotide probe SEQ ID NO 1318.

XX KW Human; probe; ss; array element; Parkinson's disease;

XX KW signalling pathway population; cancer; adenocarcinoma; leukaemia;

XX KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.

XX OS Homo sapiens.

XX PN US6500938-B1.

XX PD 31-DEC-2002.

XX PF 30-JAN-1998; 98US-0016434.

XX PR 30-JAN-1998; 98US-0016434.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Au-Young J, Seilhamer JJ;

XX WPI; 2003-352189/33.

XX CC Combination of polynucleotide probes, useful as array elements in a
XX CC microarray for monitoring the expression of a number of target
XX CC polynucleotides -

XX PS Claim 1; SEQ ID NO 1318; 65pp; English.

XX CC The invention relates to a combination which, comprises a number of
XX CC polynucleotide probes comprising a sequence selected from one of the 1490
XX CC sequences mentioned in the specification. The combination is useful as an
XX CC array element in a microarray for monitoring the expression of a number
XX CC of target polynucleotides. The microarray is particularly useful in the
XX CC diagnosis and treatment of cancer and immunopathology and neuropathology.
XX CC The microarray is useful in diagnostics and treatment regimens, drug
XX CC discovery and pharmacogenomics. The microarray is also useful for
XX CC monitoring progression of diseases and for developing sophisticated
XX CC profiles for the effects of currently available therapeutic drugs. The
XX CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
XX CC and genomic fragments and in research and diagnostic applications. The
XX CC array can detect changes in expression in a large number of genes coding
XX CC for different signalling pathway populations which can be used to diagnose
XX CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
XX CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
XX CC and Parkinson's disease. The present sequence represents a polynucleotide
XX CC probe of the invention.
XX CC Note: the sequence data for this patent did not form part of the printed
XX CC specification but was obtained in electronic format directly from USPTO
XX CC at seqdata.uspto.gov/sequence.html?DocID=96500938B1.

[illegible]

XX OS Homo sapiens.
XX PN WO200194629-A2.
XX PD 13-DEC-2001.
XX PF 30-MAY-2001; 2001WO-US10838.
XX XX 05-JUN-2000; 2000US-209473P.
XX PR 05-JUN-2000; 2000US-209531P.
XX PR 18-SEP-2000; 2000US-233133P.
XX PR 18-SEP-2000; 2000US-233617P.
XX PR 20-SEP-2000; 2000US-234009P.
XX PR 20-SEP-2000; 2000US-234034P.
XX PR 20-SEP-2000; 2000US-234052P.
XX PR 22-SEP-2000; 2000US-234509P.
XX PR 22-SEP-2000; 2000US-234567P.
XX PR 25-SEP-2000; 2000US-234923P.
XX PR 25-SEP-2000; 2000US-235077P.
XX PR 25-SEP-2000; 2000US-235082P.
XX PR 25-SEP-2000; 2000US-235134P.
XX PR 25-SEP-2000; 2000US-235280P.
XX PR 26-SEP-2000; 2000US-235280P.
XX PR 26-SEP-2000; 2000US-235637P.
XX PR 26-SEP-2000; 2000US-235638P.
XX PR 27-SEP-2000; 2000US-235711P.
XX PR 27-SEP-2000; 2000US-235720P.
XX PR 27-SEP-2000; 2000US-235840P.
XX PR 27-SEP-2000; 2000US-235863P.
XX PR 28-SEP-2000; 2000US-236028P.
XX PR 28-SEP-2000; 2000US-236032P.
XX PR 28-SEP-2000; 2000US-236033P.
XX PR 28-SEP-2000; 2000US-236034P.
XX PR 28-SEP-2000; 2000US-236109P.
XX PR 28-SEP-2000; 2000US-236111P.
XX PR 29-SEP-2000; 2000US-236842P.
XX PR 29-SEP-2000; 2000US-244567P.
XX PR 01-NOV-2000; 2000US-245084P.
XX PA (AVAL-) AVALON PHARM.
XX XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
XX PI Soppet DR, Weaver Z;
XX XX WPI; 2002-198254/24.
XX XX Screening for anti-neoplastic agent involves exposing cells to a
XX PT chemical agent to be tested for anti-neoplastic activity, and
XX PT determining a change in expression of a gene of a signature gene set
XX XX Claim 1; SEQ ID 716; 44pp; English.
XX XX The present invention describes a method (M1) for screening for an
XX CC anti-neoplastic agent. The method involves exposing cells to a chemical
XX CC agent to be tested for anti-neoplastic activity, determining a change in
XX CC expression of at least one gene (I) of a signature gene set, where (I)
XX CC comprises a sequence (S) selected from 847 sequences (given in AB61664
XX CC to AB61664), or is at least 95% identical to (S), where a change in
XX CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
XX CC activity and can be used in gene therapy. M1 can be used for screening

CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer.
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilm's tumour.
XX XX Sequence 3196 BP; 833 A; 762 C; 789 G; 812 T; 0 other;
SQ Query Match 100.0%; Score 21; DB 24; Length 3196;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTGGCGGAGTTGGGGGCT 21
Db 2891 GCTGGCGGAGTTGGGGGCT 2871
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ID ABL69294 standard; DNA; 3196 BP.
XX AC ABL69294;
XX XX 15-MAY-2002 (first entry)
DT DT
XX XX
DE DE
XX XX Prostate cancer related gene sequence SEQ ID NO:7631.
XX XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX OS Homo sapiens.
XX XX WO200194629-A2.
XX XX 13-DEC-2001.
XX XX 30-MAY-2001; 2001WO-US10838.
XX PR 05-JUN-2000; 2000US-209473P.
XX PR 05-JUN-2000; 2000US-209531P.
XX PR 18-SEP-2000; 2000US-233133P.
XX PR 18-SEP-2000; 2000US-233617P.
XX PR 20-SEP-2000; 2000US-234009P.
XX PR 20-SEP-2000; 2000US-234034P.
XX PR 20-SEP-2000; 2000US-234052P.
XX PR 22-SEP-2000; 2000US-234509P.
XX PR 22-SEP-2000; 2000US-234567P.
XX PR 25-SEP-2000; 2000US-234923P.
XX PR 25-SEP-2000; 2000US-235077P.
XX PR 25-SEP-2000; 2000US-235082P.
XX PR 25-SEP-2000; 2000US-235134P.
XX PR 25-SEP-2000; 2000US-235280P.
XX PR 26-SEP-2000; 2000US-235280P.
XX PR 26-SEP-2000; 2000US-235638P.
XX PR 27-SEP-2000; 2000US-235711P.
XX PR 27-SEP-2000; 2000US-235720P.
XX PR 27-SEP-2000; 2000US-235840P.
XX PR 27-SEP-2000; 2000US-235863P.
XX PR 28-SEP-2000; 2000US-236028P.
XX PR 28-SEP-2000; 2000US-236032P.
XX PR 28-SEP-2000; 2000US-236033P.
XX PR 28-SEP-2000; 2000US-236034P.
XX PR 28-SEP-2000; 2000US-236109P.
XX PR 28-SEP-2000; 2000US-236111P.
XX PR 29-SEP-2000; 2000US-236842P.
XX PR 29-SEP-2000; 2000US-244567P.
XX PR 01-NOV-2000; 2000US-245084P.
XX PA (AVAL-) AVALON PHARM.
XX XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
XX PI Soppet DR, Weaver Z;
XX XX WPI; 2002-198254/24.
XX XX Screening for anti-neoplastic agent involves exposing cells to a
XX PT chemical agent to be tested for anti-neoplastic activity, and
XX PT determining a change in expression of a gene of a signature gene set
XX XX Claim 1; SEQ ID 716; 44pp; English.
XX XX The present invention describes a method (M1) for screening for an
XX CC anti-neoplastic agent. The method involves exposing cells to a chemical
XX CC agent to be tested for anti-neoplastic activity, determining a change in
XX CC expression of at least one gene (I) of a signature gene set, where (I)
XX CC comprises a sequence (S) selected from 847 sequences (given in AB61664
XX CC to AB61664), or is at least 95% identical to (S), where a change in
XX CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
XX CC activity and can be used in gene therapy. M1 can be used for screening

PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237315P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
XX (AVAL-) AVALON PHARM.
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX WPI; 2002-188264/24.
XX Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set -
XX Claim 1; SEQ ID 7631; 44pp; English.
XX The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC esophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilm's tumour.
XX Sequence 3196 BP; 833 A; 762 C; 789 G; 812 T; 0 other;
SQ Query Match 100.0%; Score 21; DB 24; Length 3196;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTGGCGGAGTTGGGGCCT 21
Db 2891 GCTGGCGGAGTTGGGGCCT 2871
RESULT 10
ABN99663/c
ID ABN99663 standard; DNA; 8133 BP.
XX AC ABN99663;
XX AC ABN99663;
XX 16-AUG-2002 (first entry)
XX Human clusterin gene sequence 2.
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;
XX hypercholesterolaemia; cardiovascular disorder; ds;
XX hyperproliferative disorder; hyperlipidemic disorder.
XX Homo sapiens.
XX WO200222635-A1.
PS

XX 21-MAR-2002.
PD 10-SEP-2001; 2001WO-US28235.
XX 11-SEP-2000; 2000US-06S9791.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Freier SM;
XX WPI; 2002-404805/43.
XX Novel antisense compound targeted to nucleic acid molecule encoding
PT clusterin, useful for treating animal having disease associated with
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder -
XX Example 15; Page 93-98; 125pp; English.
XX The invention comprises antisense oligonucleotides that are capable of
CC inhibiting expression of the human clusterin gene. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of clusterin in cells. The antisense oligonucleotides are also
CC useful for treating an animal with a disease or condition associated with
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
CC hyperproliferative disorders; and hyperlipidemic disorders). The present
CC DNA sequence represents a human clusterin gene sequence.
XX Sequence 8133 BP; 1982 A; 2024 C; 2002 G; 2125 T; 0 other;
SQ Query Match 100.0%; Score 21; DB 24; Length 8133;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTGGCGGAGTTGGGGCCT 21
Db 7752 GCTGGCGGAGTTGGGGCCT 7732
RESULT 11
ABL80072
ID ABL80072 standard; cDNA; 250 BP.
XX AC ABL80072;
XX 17-MAY-2002 (first entry)
XX Human ovarian cancer related cDNA clone SEQ ID NO:3050.
XX Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
XX Homo sapiens.
XX WO200192581-A2.
XX 06-DEC-2001.
XX 29-MAY-2001; 2001WO-US17756.
XX 26-MAY-2000; 2000US-207484P.
XX (CORI-) CORIXA CORP.
XX Algate PA, Harlocker SL, Jones R;
XX WPI; 2002-122075/16.
XX Composition for therapy and diagnosis of ovarian cancer comprising
PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
PT polypeptide, antibody specific to polypeptide or T cell expressing
PT polypeptide -
XX Claim 1; SEQ ID 3050; 489pp; English.
PS

PT production of enzymes, secondary metabolites or other commercially and
 PT medically useful products -

PS Disclosure; Page 63-64; 71pp; English.

XX The present invention relates to novel fungal gene expression regulators
 CC (ABQ94217-ABQ94285 and ABP63084-ABP63152). An01, An05, An09, An10, An13,
 CC An17, An20, An28, An34, At01-2, At03, At05, At07, At08, At11,
 CC At14, At16, At18, At19, At20, At22, At24, At27, At32, At35, At36, At37,
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 CC At1962, At1963, At1964, At1965, At1966, At1967, At1968, At1969, At1970,
 CC At1971, At1972, At1973, At1974, At1975, At1976, At1977, At1978, At1979,
 CC At1980, At1981, At1982, At1983, At1984, At1985, At1986, At1987, At1988,
 CC At1989, At1990, At1991, At1992, At1993, At1994, At1995, At1996, At1997,
 CC At1998, At1999, At2000, At2001, At2002, At2003, At2004, At2005, At2006,
 CC At2007, At2008, At2009, At2010, At2011, At2012, At2013, At2014, At2015,
 CC At2016, At2017, At2018, At2019, At2020, At2021, At2022, At2023, At2024,<

XX Claim 2; Fig 15; 156pp; English.
PS
XX AAH25131-35 encode human alcohol dehydrogenase proteins, designated
CC 21620, 33756, 21676, 21612 and 21615, respectively. Alcohol dehydrogenase
CC polynucleotides and polypeptides are useful for treatment and diagnosis
CC of disorders mediated by or related to alcohol dehydrogenase. They can
CC be used for treating disorders of colon, brain, skin, heart, blood
CC vessels, kidney, prostate, skeletal muscle, ovary, testis and epididymis,
CC spleen, lung, liver, uterus and endometrium, T-cells, red cells, thymus,
CC B cells, breast, thyroid, pancreas, small intestine, reduced platelet
CC number, precursor T cell neoplasms, bone forming cells, and bone marrow
CC cells.
XX
SQ Sequence 2535 BP; 720 A; 531 C; 537 G; 695 T; 52 other;

Query Match 80.0%; Score 16.8; DB 22; Length 2535;
Best Local Similarity 90.0%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGGCGGGAGTTGGGGCC 20
Db 73 GATGGCGGGAGTTAGGGCC 54

Search completed: January 21, 2004, 11:44:48
Job time : 151 secs

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Sequence 101667, Ap
Sequence 3050, App
Sequence 300, App
Sequence 346, App
Sequence 1, Appl
Sequence 28214, A
Sequence 33, Appl
Sequence 109, App
Sequence 1887, App
Sequence 8, Appl
Sequence 236, App
Sequence 1054, Ap
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Sequence 169, App
Sequence 590, App
Sequence 66, Appl
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Sequence 9, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 5, Appl
Sequence 13, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 23, Appl
Sequence 10, Appl
Sequence 13, Appl

16 18.4 87.6 2257 14 US-10-027-632-101667
17 17.8 84.8 250 10 US-09-867-701-3050
18 17.8 84.8 1236 15 US-10-156-761-300
19 17.8 84.8 1236 15 US-10-156-761-346
20 17.8 84.8 9025608 15 US-10-156-761-1
21 17.4 82.9 441 11 US-09-918-995-28214
22 17.4 82.9 3845 14 US-10-029-180-33
23 17.4 82.9 3732 14 US-10-029-180-109
24 16.8 80.0 1370 12 US-10-104-047-1887
25 16.8 80.0 2535 9 US-09-796-089-8
26 16.8 80.0 4196 13 US-10-120-988-236
27 16.8 80.0 14654 9 US-09-764-860-1054
28 16.8 80.0 14854 13 US-10-213-872-1054
29 16.8 80.0 14854 15 US-10-074-095-1054
30 16.8 80.0 28350 12 US-10-085-117-169
31 16.4 78.1 50 11 US-09-993-346-590
32 16.4 78.1 68 10 US-09-875-082-66
33 16.4 78.1 68 11 US-09-875-082-66
34 16.4 78.1 144 15 US-10-219-450-6
35 16.4 78.1 226 14 US-10-125-086-9
36 16.4 78.1 226 15 US-10-178-109-9
37 16.4 78.1 226 15 US-10-123-087-9
38 16.4 78.1 243 13 US-10-066-218-5
39 16.4 78.1 256 9 US-09-126-945B-13
40 16.4 78.1 256 9 US-09-739-907-10
41 16.4 78.1 256 9 US-09-729-835-10
42 16.4 78.1 256 9 US-09-739-254-10
43 16.4 78.1 256 9 US-09-731-816-23
44 16.4 78.1 256 9 US-09-768-826-10
45 16.4 78.1 256 9 US-09-726-348-13

ALIGNMENTS

RESULT 1
US-09-944-326-12
Sequence 12, Application US/09944326
Patent No. US20020128220A1
GENERAL INFORMATION:
APPLICANT: Gleave, Martin
APPLICANT: Rennie, Paul S.
APPLICANT: Miyake, Hideaki
APPLICANT: Nelson, Colleen
TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
FILE REFERENCE: USC P-020-2
CURRENT APPLICATION NUMBER: US/09/944,326
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 60/121,726
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 09/913,325
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 21
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
OTHER INFORMATION: antisense TRPM-2 ODN
US-09-944-326-12

Query Match 100.0%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGGGGAGTTGGGGGCT 21
DB 1 GCTGGGGGAGTTGGGGGCT 21

RESULT 2
US-09-967-736A-12

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	21	100.0	21	13	US-09-967-726A-12
3	21	100.0	21	13	US-10-080-794-12
4	21	100.0	450	11	US-09-918-995-759
5	21	100.0	505	10	US-09-833-381-159
6	21	100.0	1495	13	US-10-210-120-74
7	21	100.0	1678	10	US-09-765-231A-16
8	21	100.0	1775	13	US-10-133-033-243
9	21	100.0	2876	15	US-10-116-255-17
10	21	100.0	3196	10	US-09-969-708-160
11	21	100.0	3196	13	US-09-873-367C-716
12	19.4	92.4	403	10	US-09-833-381-444
13	19.4	92.4	525	10	US-09-833-381-443
14	19.4	92.4	4283	13	US-09-814-353-19511
15	18.4	87.6	2257	13	US-10-027-632-101667

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; Sequence 12, Application US/09967726A
; Publication No. US20030158130A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Zellweger, Tobias
; TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2
; FILE REFERENCE: UBC-P-022
; CURRENT APPLICATION NUMBER: US/09/967,726A
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
; US-09-967-726A-12

Query Match      100.0%; Score 21; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGCCT 21
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Db 1 GCTGGCGGAGTTGGGGCCT 21

RESULT 3
US-10-080-794-12
; Sequence 12, Application US/10080794
; Publication No. US20030166591A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE
; FILE REFERENCE: UBC-P-020-3
; CURRENT APPLICATION NUMBER: US/10/080,794
; CURRENT FILING DATE: 2002-02-22
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/944,326
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
; US-10-080-794-12

Query Match      100.0%; Score 21; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGCCT 21
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Db 1 GCTGGCGGAGTTGGGGCCT 21

RESULT 4
US-09-918-995-759/c
; Sequence 759, Application US/09918995

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; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 759
; LENGTH: 450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(450)
; OTHER INFORMATION: n = A,T,C or G
; US-09-918-995-759

Query Match      100.0%; Score 21; DB 11; Length 450;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGCCT 21
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Db 303 GCTGGCGGAGTTGGGGCCT 283

RESULT 5
US-09-833-381-159
; Sequence 159, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NO US20020132090A1el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 159
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-833-381-159

Query Match      100.0%; Score 21; DB 10; Length 505;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGCCT 21
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Db 105 GCTGGCGGAGTTGGGGCCT 125

RESULT 6
US-10-210-120-74/c
; Sequence 74, Application US/10210120
; Publication No. US20030175736A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Ruben, Mark A.
; APPLICANT: Sreekumar, Arun
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; FILE REFERENCE: UM-07221
; CURRENT APPLICATION NUMBER: US/10/210,120
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/309,581

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; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 6/334,468
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 74
; LENGTH: 1495
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-120-74

Query Match      100.0%; Score 21; DB 13; Length 1495;
Best Local Similarity 100.0%; Pred. No. 4.4; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
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Db 1388 GCTGGCGGAGTTGGGGCCT 1368

RESULT 7
US-09-765-231A-16/c
; Sequence 16, Application US/09765231A
; Patent No. US20020119452A1
; GENERAL INFORMATION:
; APPLICANT: Searle/Monsanto
; APPLICANT: Phippard, Deborah
; APPLICANT: Vasanthakumari, Geetha
; APPLICANT: Dotson, Stanton
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Osteoarthritis tissue-derived nucleic acids, polypeptides,
; TITLE OF INVENTION: vectors, and cells
; FILE REFERENCE: SO-3221 PR
; CURRENT APPLICATION NUMBER: US/09/765,231A
; CURRENT FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 82
; SEQ ID NO 16
; LENGTH: 1678
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-765-231A-16

Query Match      100.0%; Score 21; DB 10; Length 1678;
Best Local Similarity 100.0%; Pred. No. 4.3; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
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Db 1558 GCTGGCGGAGTTGGGGCCT 1538

RESULT 8
US-10-133-013-243/c
; Sequence 243, Application US/10133013
; Publication No. US2003016903A1
; GENERAL INFORMATION:
; APPLICANT: Astronoff, Anna
; APPLICANT: Bandman, Olga
; APPLICANT: Cocks, Benjamin G.
; TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
; FILE REFERENCE: PA-0049 US
; CURRENT APPLICATION NUMBER: US/10/133,013
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/287,067
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PERL Program
; SEQ ID NO 243
; LENGTH: 1775
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. US2003016903A1 2966620cB1
US-10-133-013-243

Query Match      100.0%; Score 21; DB 13; Length 1775;
Best Local Similarity 100.0%; Pred. No. 4.2; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
   |||||
Db 1650 GCTGGCGGAGTTGGGGCCT 1630

RESULT 9
US-10-116-255-17/c
; Sequence 17, Application US/10116255
; Publication No. US20030036646A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Uncoupling Protein Polynucleotides, Polypeptides, and
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: PT009F1
; CURRENT APPLICATION NUMBER: US/10/116,255
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/685,897
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: PCT/US00/09534
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,701
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/142,821
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/149,448
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: 60/164,751
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 2876
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-116-255-17

Query Match      100.0%; Score 21; DB 15; Length 2876;
Best Local Similarity 100.0%; Pred. No. 3.8; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
   |||||
Db 2734 GCTGGCGGAGTTGGGGCCT 2714

RESULT 10
US-09-969-708-160/c
; Sequence 160, Application US/09969708
; Patent No. US20020102532A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-70
; CURRENT APPLICATION NUMBER: US/09/969,708
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: US/60/237,606
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,608
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,425
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 658
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 160
; LENGTH: 3196
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-969-708-160

Query Match
Best Local Similarity 100.0%; Score 21; DB 10; Length 3196;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
    |||||
Db 2891 GCTGGCGGAGTTGGGGCCT 2871

RESULT 11
US-09-873-367C-716/C
; Sequence 716, Application US/09873367C
; Publication No. US20030165839A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; APPLICANT: Soppet, Daniel
; APPLICANT: Endress, Gregory
; APPLICANT: Augustus, Mesna
; APPLICANT: Ebner, Reinhard
; APPLICANT: Carter, Kenneth
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: 689290-64
; CURRENT APPLICATION NUMBER: US/09/873,367C
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,891
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,842
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/244,867
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: U.S. 60/245,084
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 1067
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 716
; LENGTH: 3196
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-367C-716

Query Match
Best Local Similarity 100.0%; Score 21; DB 13; Length 3196;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
    |||||
Db 2891 GCTGGCGGAGTTGGGGCCT 2871

RESULT 12
US-09-833-381-444
; Sequence 444, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NO. US20020132090A1el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 444
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-444

Query Match
Best Local Similarity 92.4%; Score 19.4; DB 10; Length 403;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
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Db 102 GCTGGCGGAGTTGGGGCCT 122

RESULT 13
US-09-833-381-443
; Sequence 443, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NO. US20020132090A1el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 443
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-443

Query Match
Best Local Similarity 92.4%; Score 19.4; DB 10; Length 525;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
    |||||
Db 106 GCTGGCGGAGTTGGGGCCT 126

RESULT 14
US-09-814-353-19511/c
; Sequence 19511, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19511
; LENGTH: 4283
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-19511
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Wed Jan 21 15:56:31 2004

Query Match 92.4%; Score 19.4; DB 13; Length 4283;
Best Local Similarity 95.2%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
DB 1490 GCTGGCGGAGTTGGGGCCT 1470

RESULT 15

US-10-027-632-101667
; Sequence 101667, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101667
; LENGTH: 2257
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-101667

Query Match 87.6%; Score 18.4; DB 13; Length 2257;
Best Local Similarity 95.0%; Pred. No. 50;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCGGAGTTGGGGCCT 21
DB 1340 CTGGCTGAGTTGGGGCCT 1359

Search completed: January 21, 2004, 15:35:50
Job time : 224 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 11:34:17 ; Search time 56 Seconds
(without alignments)
165.519 Million cell updates/sec

Title: US-09-913-325-12
Perfect score: 21
Sequence: 1 gctggcgagtggtggcgct 21

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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3: /cgn2_6/ptodata/2/ina/5A-COMB.seq.*
4: /cgn2_6/ptodata/2/ina/5B-COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS-COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
C 1	21	100.0	1416	US-09-016-434-1318	Sequence 1318, Ap
C 2	21	100.0	1648	US-09-659-791A-3	Sequence 3, Appl
C 3	21	100.0	8133	US-09-659-791A-10	Sequence 10, Appl
C 4	16.8	80.0	3562	US-09-360-197-1	Sequence 1, Appl
C 5	16.8	80.0	3647	US-09-360-197-7	Sequence 7, Appl
C 6	16.4	78.1	50	US-08-171-389-590	Sequence 590, App
C 7	16.4	78.1	50	US-08-123-936-590	Sequence 590, App
C 8	16.4	78.1	50	US-08-475-228A-590	Sequence 590, App
C 9	16.4	78.1	50	US-08-482-080A-590	Sequence 590, App
C 10	16.4	78.1	50	US-09-354-947-590	Sequence 590, App
C 11	16.4	78.1	50	PCT-US93-12388-590	Sequence 590, App
C 12	16.4	78.1	68	US-08-790-963-66	Sequence 66, Appl
C 13	16.4	78.1	68	US-09-371-774-66	Sequence 66, Appl
C 14	16.4	78.1	226	US-09-659-026A-9	Sequence 9, Appl
C 15	16.4	78.1	256	US-09-106-182-24	Sequence 24, Appl
C 16	16.4	78.1	256	US-09-227-357-10	Sequence 10, Appl
C 17	16.4	78.1	256	US-09-280-839-13	Sequence 13, Appl
C 18	16.4	78.1	256	US-09-411-977-24	Sequence 24, Appl
C 19	16.4	78.1	256	US-09-479-729B-30	Sequence 30, Appl
C 20	16.4	78.1	256	US-09-257-179-10	Sequence 10, Appl
C 21	16.4	78.1	256	US-09-149-476-10	Sequence 10, Appl
C 22	16.4	78.1	256	US-09-288-143-10	Sequence 10, Appl
C 23	16.4	78.1	256	US-09-487-792-32	Sequence 32, Appl
C 24	16.4	78.1	256	US-09-152-060-10	Sequence 10, Appl
C 25	16.4	78.1	256	US-09-908-594-32	Sequence 32, Appl
C 26	16.4	78.1	256	US-09-461-325-10	Sequence 10, Appl
C 27	16.4	78.1	256	US-09-489-847-10	Sequence 10, Appl

C 28	16.4	78.1	256	4	US-09-231-788-26	Sequence 26, Appl
C 29	16.4	78.1	256	4	US-09-512-363-27	Sequence 27, Appl
C 30	16.4	78.1	256	4	US-09-176-200-27	Sequence 27, Appl
C 31	16.4	78.1	256	4	US-08-205-258-10	Sequence 10, Appl
C 32	16.4	78.1	256	4	US-09-690-454-10	Sequence 10, Appl
C 33	16.4	78.1	256	4	US-09-482-271-19	Sequence 19, Appl
C 34	16.4	78.1	256	4	US-09-482-273-10	Sequence 10, Appl
C 35	16.4	78.1	256	4	US-09-904-615-10	Sequence 10, Appl
C 36	16.4	78.1	256	4	US-09-369-247-10	Sequence 10, Appl
C 37	16.4	78.1	271	3	US-09-106-182-18	Sequence 18, Appl
C 38	16.4	78.1	271	4	US-09-227-357-5	Sequence 5, Appl
C 39	16.4	78.1	271	4	US-09-280-839-8	Sequence 8, Appl
C 40	16.4	78.1	271	4	US-09-411-977-20	Sequence 20, Appl
C 41	16.4	78.1	271	4	US-09-479-729B-25	Sequence 25, Appl
C 42	16.4	78.1	271	4	US-09-257-179-5	Sequence 5, Appl
C 43	16.4	78.1	271	4	US-09-149-476-5	Sequence 5, Appl
C 44	16.4	78.1	271	4	US-09-288-143-5	Sequence 5, Appl
C 45	16.4	78.1	271	4	US-09-487-792-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-09-016-434-1318/c
; Sequence 1318, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 895-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1318:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1416 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g338056
; US-09-016-434-1318

Query Match 100.0%; Score 21; DB 4; Length 1416;
Best Local Similarity 100.0%; Pred. No. 2.1;

RESULT 6
US-08-171-389-590/c
; Sequence 590, Application US/08171389
; Patent No. 5578444
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.

APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/171,389
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 590:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start
INDIVIDUAL ISOLATE: site 31)
US-08-171-389-590

Query Match 78.1%; Score 16.4; DB 1; Length 50;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCGGAGTTGGGGC 19
|||||
DB 20 CTGGCGGAGTTAGGGC 3

RESULT 7

US-08-123-936-590/c
Sequence 590, Application US/08123936
Patent No. 5726014
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.

TITLE OF INVENTION: Screening Assay for the Detection of
TITLE OF INVENTION: DNA-Binding Molecules
NUMBER OF SEQUENCES: 640
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/123,936
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 590:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start
INDIVIDUAL ISOLATE: site 31)
US-08-123-936-590

RESULT 8

US-08-475-228A-590/c
Sequence 590, Application US/08475228A
Patent No. 5869241
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.

QY 2 CTGGCGGAGTTGGGGC 19
|||||
DB 20 CTGGCGGAGTTAGGGC 3

Query Match 78.1%; Score 16.4; DB 1; Length 50;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,228A
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,936
; FILING DATE: 17-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/996,783
; FILING DATE: 23-DEC-1992
; APPLICATION NUMBER: US 07/723,618
; FILING DATE: 27-JUN-1991
; APPLICATION NUMBER: US 08/081,070
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 590:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start
; INDIVIDUAL ISOLATE: site 31)
; US-08-475-228A-590

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Query Match      78.1%; Score 16.4; DB 2; Length 50;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 2 CTGGCGGAGTTGGGGC 19
Db 20 CTGGCGGAGTTAGGGC 3

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RESULT 9
US-08-482-080A-590/c
; Sequence 590, Application US/08482080A
; Patent No. 6010849
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; APPLICANT: Fry, Kirk E.
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; NUMBER OF SEQUENCES: 664
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,080A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/171,389
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: US 08/123,936
; FILING DATE: 17-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/996,783
; FILING DATE: 23-DEC-1992
; APPLICATION NUMBER: US 07/723,618
; FILING DATE: 27-JUN-1991
; APPLICATION NUMBER: US 08/081,070
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brady, John F.
; REGISTRATION NUMBER: 39,118
; REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 324-0880
; TELEFAX: (650) 324-0960
; INFORMATION FOR SEQ ID NO: 590:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start
; INDIVIDUAL ISOLATE: site 31)
; US-08-482-080A-590

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Query Match      78.1%; Score 16.4; DB 3; Length 50;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 2 CTGGCGGAGTTGGGGC 19
Db 20 CTGGCGGAGTTAGGGC 3

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RESULT 10
US-09-354-947-590/c
; Sequence 590, Application US/09354947
; Patent No. 6384208
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; APPLICANT: Fry, Kirk E.
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; NUMBER OF SEQUENCES: 664
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/354,947
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,080
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Brady, John F.
REGISTRATION NUMBER: 39,118
REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 590:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start
INDIVIDUAL ISOLATE: site 31)
US-09-354-947-590

Query Match 78.1%; Score 16.4; DB 4; Length 50;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCGGAGTTGGGGC 19
||| ||||| ||||| |||||
DB 20 CTGGCGGAGTTGGGGC 3

RESULT 11
PCT-US93-12388-590/c
Sequence 590, Application PC/TUS9312388
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Fenobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12388
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 590:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start
INDIVIDUAL ISOLATE: site 31)
PCT-US93-12388-590

Query Match 78.1%; Score 16.4; DB 5; Length 50;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCGGAGTTGGGGC 19
||| ||||| ||||| |||||
DB 20 CTGGCGGAGTTGGGGC 3

RESULT 12
US-08-790-963-66
Sequence 66, Application US/08790963
Patent No. 5837464
GENERAL INFORMATION:
APPLICANT: Daniel J. Capon
TITLE OF INVENTION: Compositions and Methods For
TITLE OF INVENTION: Determining Anti-viral Drug Susceptibility And
TITLE OF INVENTION: Resistance
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/790,963
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50130-B/JPW/AKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 base pairs

; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 US-08-790-963-66

Query Match 78.1%; Score 16.4; DB 2; Length 68;
 Best Local Similarity 94.4%; Pred. No. 1.5e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCGGAGTTGGGGC 19
 DB 33 CTGGCGGAGTTAGGGC 50

RESULT 13

US-09-371-774-66
 ; Sequence 66, Application US/09371774
 ; Patent No. 6242187

GENERAL INFORMATION:

; APPLICANT: Daniel J. Capon
 ; Christos John Petropoulos
 ; TITLE OF INVENTION: Compositions And Methods For
 ; Determining Anti-viral Drug Susceptibility And
 ; Resistance And Anti-viral Drug Screening
 ; NUMBER OF SEQUENCES: 105
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 10036

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version#1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/371,774
 ; FILING DATE: 10-Aug-1999
 ; CLASSIFICATION: <unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 50130-F/JPW/CMR
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-278-0400
 ; TELEFAX: 212-391-0526
 ; INFORMATION FOR SEQ ID NO: 66:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 68 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 66:
 US-09-371-774-66

Query Match 78.1%; Score 16.4; DB 3; Length 68;
 Best Local Similarity 94.4%; Pred. No. 1.5e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCGGAGTTGGGGC 19
 DB 33 CTGGCGGAGTTAGGGC 50

RESULT 14

US-09-659-026A-9/c
 ; Sequence 9, Application US/09659026A
 ; Patent No. 6461616

GENERAL INFORMATION:

; APPLICANT: MONTELABO, Ronald
 ; APPLICANT: CRAIGO, Jodi K.
 ; APPLICANT: ISSEL, Charles
 ; APPLICANT: PUFFER, Bridget
 ; APPLICANT: HENNESSY, Kristina J.
 ; APPLICANT: BROWN, Karen K.
 ; TITLE OF INVENTION: EIAV P26 DELETION VACCINE AND DIAGNOSTIC
 ; FILE REFERENCE: MONTELABO ET AL.
 ; CURRENT APPLICATION NUMBER: US/09/659,026A
 ; CURRENT FILING DATE: 2001-06-11
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 9
 ; LENGTH: 226
 ; TYPE: DNA
 ; ORGANISM: IN VITROGEN
 US-09-659-026A-9

Query Match 78.1%; Score 16.4; DB 4; Length 226;
 Best Local Similarity 94.4%; Pred. No. 1.6e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCGGAGTTGGGGC 19
 DB 168 CTGGCGGAGTTAGGGC 151

RESULT 15

US-09-106-182-24/c
 ; Sequence 24, Application US/09106182
 ; Patent No. 6046035
 ; GENERAL INFORMATION:
 ; APPLICANT: Shi, Yanggu
 ; APPLICANT: Ruben, Steve
 ; TITLE OF INVENTION: Cardiotrophin-Like Cytokine
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc
 ; STREET: 9410 Key West Ave
 ; CITY: Rockville
 ; STATE: MD
 ; COUNTRY: US
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/106,182
 ; FILING DATE: Herewith
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/051,053
 ; FILING DATE: 30-JUN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brookes, A. Anders
 ; REGISTRATION NUMBER: 36,373
 ; REFERENCE/DOCKET NUMBER: PF385
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 301-309-8504
 ; TELEFAX: 301-309-8439
 ; INFORMATION FOR SEQ ID NO: 24:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 256 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 US-09-106-182-24

Query Match 78.1%; Score 16.4; DB 3; Length 256;
 Best Local Similarity 94.4%; Pred. No. 1.6e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTGGCGGAGTTGGGGC 19
| | | | | | | | | |
Db 123 CTGGCGGAGTTAGGGC 106

Search completed: January 21, 2004, 13:11:50
Job time : 58 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 10:59:47 ; Search time 1733 Seconds
(without alignments)
294.515 Million cell updates/sec

Title: US-09-913-325-12
Perfect score: 21
Sequence: 1 gctggggagctggggccct 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estm:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_pig:*
27: em_gss_vri:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	21	100.0	121	14	H84500 yv02d12.s1
2	21	100.0	121	14	R93611 YG38d11.s1
3	21	100.0	135	14	TS3781 Y083e02.s1
4	21	100.0	143	10	BE765434 IL3-NT010

5	21	100.0	145	10	AW904670
6	21	100.0	146	9	AA738045
7	21	100.0	150	13	BU728259
8	21	100.0	151	9	AA434384
9	21	100.0	151	12	BI055204
10	21	100.0	153	12	BI040715
11	21	100.0	157	12	BI467181
12	21	100.0	159	12	BI040516
13	21	100.0	169	9	AI523434
14	21	100.0	169	9	AI691105
15	21	100.0	171	10	BF897129
16	21	100.0	171	10	BF919288
17	21	100.0	172	9	AA235650
18	21	100.0	172	10	BF932077
19	21	100.0	174	9	AA635704
20	21	100.0	174	10	BF374244
21	21	100.0	174	10	BE702836
22	21	100.0	176	10	BF364496
23	21	100.0	176	12	BI040542
24	21	100.0	177	12	BI040538
25	21	100.0	179	10	AW868593
26	21	100.0	179	12	BI040710
27	21	100.0	181	12	BI040535
28	21	100.0	182	10	AW868587
29	21	100.0	183	14	CB048333
30	21	100.0	183	14	CB048334
31	21	100.0	184	9	AA433884
32	21	100.0	185	12	BM994290
33	21	100.0	185	14	R83374
34	21	100.0	187	10	AW897945
35	21	100.0	187	10	BE765800
36	21	100.0	187	10	BE766185
37	21	100.0	188	13	BU734617
38	21	100.0	190	10	BF749857
39	21	100.0	193	12	BI040729
40	21	100.0	195	10	AW904698
41	21	100.0	196	10	BF749861
42	21	100.0	196	12	BI040731
43	21	100.0	196	12	BI055202
44	21	100.0	198	9	AW243998
45	21	100.0	198	10	AW868592

ALIGNMENTS

RESULT 1
H84500
LOCUS
DEFINITION yv02d12.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:241559 3' similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN);
mRNA sequence.
H84500 121 bp mRNA linear EST 13-NOV-1995
IMAGE:241559 3' similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN);
mRNA sequence.
H84500 1 GI:1063171
VERSION H84500.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1

High quality sequence stops: 1
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: Promega -2iml3
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

source

```

1. 121
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="GDB:3790692"
  /db_xref="taxon:9606"
  /clone="IMAGE:241559"
  /sex="male"
  /dev_stage="20 week-post conception fetus"
  /lab_host="DH10B (ampicillin resistant)"
  /clone_lib="Soares fetal liver spleen INFLS"
  /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
  with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
  1st strand cDNA was primed with a Pac I - oligo(dT) primer
  [5', AACTGGAAGAAATTAATAAGATCTTTTCTTTTCTTTT 3'],
  double-stranded cDNA was ligated to Eco RI adaptors
  (Pharmacia), digested with Pac I and cloned into the Pac I
  and Eco RI sites of the modified pT7T3 vector. Library
  went through one round of normalization. Library
  constructed by Bento Soares and M.Fatima Bonaldo."
```

BASE COUNT
 ORIGIN

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Query Match      100.0%; Score 21; DB 14; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GCTGGCGGAGTTGGGGCCCT 21
 |||||
 Db 95 GCTGGCGGAGTTGGGGCCCT 115

RESULT 2

R93611

LOCUS YQ38d11.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
 DEFINITION IMAGE:198069 3', similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN) ;
 mRNA sequence.

ACCESSION R93611

VERSION R93611.1

KEYWORDS EST.

SOURCE R93611.1 GI:967777

ORGANISM Homo sapiens (human)

REFERENCE 1. (bases 1 to 121)

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman

M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,

Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston

R., Williamson, A., Wohlmann, P., and Wilson, R.

The WashU-Merck EST Project

Unpublished

TITLE Contact: Wilson RK

JOURNAL Washington University School of Medicine

COMMENT 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1368

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 1368 Std Error: 0.00

FEATURES

source

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1. 121
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="GDB:3767119"
  /db_xref="taxon:9606"
  /clone="IMAGE:198069"
  /sex="male"
  /dev_stage="20 week-post conception fetus"
  /lab_host="DH10B (ampicillin resistant)"
  /clone_lib="Soares fetal liver spleen INFLS"
  /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
  with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
  1st strand cDNA was primed with a Pac I - oligo(dT) primer
  [5', AACTGGAAGAAATTAATAAGATCTTTTCTTTTCTTTT 3'],
  double-stranded cDNA was ligated to Eco RI adaptors
  (Pharmacia), digested with Pac I and cloned into the Pac I
  and Eco RI sites of the modified pT7T3 vector. Library
  went through one round of normalization. Library
  constructed by Bento Soares and M.Fatima Bonaldo."
```

BASE COUNT
 ORIGIN

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Query Match      100.0%; Score 21; DB 14; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GCTGGCGGAGTTGGGGCCCT 21
 |||||
 Db 85 GCTGGCGGAGTTGGGGCCCT 105

RESULT 3

T53781

LOCUS

DEFINITION

Yb83e02.s1 Stragene liver (#937224) Homo sapiens cDNA clone
 IMAGE:77786 3', similar to gb:X14723 CLUSTERIN PRECURSOR
 (HUMAN), mRNA sequence.

ACCESSION T53781

VERSION T53781.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 135)

AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chisapelli, B.,

Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins

M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore

B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,

Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,

Underwood, K., Wohlmann, P., Waterston, R., Wilson, R., and Marra, M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

Unpublished

TITLE Contact: Wilson RK

JOURNAL Washington University School of Medicine

COMMENT 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1905

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 1905 Std Error: 0.00

Seq primer: -2iml3

High quality sequence stop: 1.

Location/Qualifiers


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source
1. .135
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:497531"
/db_xref="taxon:9606"
/clone="IMAGE:77786"
/sex="male"
/dev_stage="49 years old"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene liver (#937224)"
/note="Organ: liver; Vector: pBluescript SK; Site 1: EcoRI
Site 2: XhoI; Cloned unidirectionally. Primer: Oligo
dr. Hepatectomy from normal male caucasian. Average insert
size: 1.1 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'
CAATTCGGCAG 3' -3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTT 3'"
BASE COUNT      30 a   23 c   48 g   32 t   2 others
ORIGIN

Query Match      100.0%; Score 21; DB 14; Length 135;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
|||||
Db 110 GCTGGCGGAGTTGGGGCCT 130

RESULT 4
BE765434/c
LOCUS      IL3-NT0104-200500-144-G04 NT0104 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION  BE765434
VERSION    BE765434.1 GI:10195358
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 143)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE      Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE    20202663
PUBMED     10737800
COMMENT    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=IL3-NT0104-200
500-144-G04&t3=2000-05-20&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence stop: 143.
Location/Qualifiers
1. .143
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NT0104"

FEATURES
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1. .145
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN1062"
/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      20 a   31 c   61 g   33 t
ORIGIN

/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      27 a   65 c   28 g   23 t
ORIGIN

Query Match      100.0%; Score 21; DB 10; Length 143;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
|||||
Db 102 GCTGGCGGAGTTGGGGCCT 82

RESULT 5
AW904670
LOCUS      AW904670 145 bp mRNA linear EST 24-MAY-2000
DEFINITION RCI-NN1062-260400-011-a09 NN1062 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW904670
VERSION    AW904670.1 GI:8068784
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 145)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE      Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE    20202663
PUBMED     10737800
COMMENT    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=RC1-NN1062-260
400-011-a09&t3=2000-04-26&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 34
High quality sequence stop: 145.
Location/Qualifiers
1. .145
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN1062"
/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      20 a   31 c   61 g   33 t
ORIGIN

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Query Match 100.0%; Score 21; DB 10; Length 145;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGGCT 21
 |||||
 Db 50 GCTGGCGGAGTTGGGGGCT 70

RESULT 6
 AA738045 146 bp mRNA linear EST 22-JAN-1998
 LOCUS
 DEFINITION nx15f08.s1 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:1256199 3', similar to gb:U14723 CLUSTERIN PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION AA738045
 VERSION
 KEYWORDS
 SOURCE EST.
 ORGANISM Homo sapiens (human)

REFERENCE
 AUTHORS
 TITLE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 COMMENT Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps@mail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 867 Std Error: 0.00
 Seq primer: -40m13 fwd. RT from Amersham
 High quality sequence stop: 1.

FEATURES
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1256199"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP GC3"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 32 a 26 c 54 g 34 t
 ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 145;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGGCT 21
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 Db 106 GCTGGCGGAGTTGGGGGCT 126

RESULT 7
 BU728259

LOCUS BU728259 150 bp mRNA linear EST 09-OCT-2002
 DEFINITION UI-E-CQ0-adv-g-07-0-UI.s1 UI-E-CQ0 Homo sapiens cDNA clone
 UI-E-CQ0-adv-g-07-0-UI 3', mRNA sequence.

ACCESSION BU728259
 VERSION
 KEYWORDS
 SOURCE EST.
 ORGANISM Homo sapiens (human)

REFERENCE
 AUTHORS
 TITLE Bonaldo,M.F., Lennon,G. and Soares,M.B.
 JOURNAL Normalization and subtraction: two approaches to facilitate gene discovery
 MEDLINE 97044477
 PUBMED 889548

COMMENT Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
 Seq primer: M13 FORWARD
 PolyA=Yes.

FEATURES
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
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 /tissue_type="optic nerve"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-E-CQ0"
 /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-CQ0 is a cDNA library containing the following tissue(s): optic nerve. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCATTAGTC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
 TAG LIB=UI-E-CQ0
 TAG TISSUE=human optic nerve
 TAG_SEQ=CCATTAGTC"

BASE COUNT 31 a 24 c 47 g 48 t
 ORIGIN

Query Match 100.0%; Score 21; DB 13; Length 150;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGGCT 21
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 Db 126 GCTGGCGGAGTTGGGGGCT 146

RESULT 8

AA434384
LOCUS zw31h1.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
IMAGE:770949 3' similar to gb:U14723 CLUSTERIN PRECURSOR (HUMAN);
RNA sequence.

ACCESSION AA434384.1 GI:2139298
VERSION AA434384
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 151)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie,
T., Waterston, R., and Wilson, R.
WashU-Merck EST Project 1997
Unpublished
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m3 fwd. ET from Amersham.

FEATURES
source
1..151
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5980822"
/db_xref="taxon:9606"
/clone="IMAGE:770949"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="PH10B (ampicillin resistant)"
/clone_lib="Soares ovary tumor NbHOT"
/note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTTACCATCTGAGTGGGACGCGGTTTCTTTTCTTTTCTTTT 3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."

BASE COUNT 32 a 27 c 56 g 36 t
ORIGIN
Query Match 100.0%; Score 21; DB 9; Length 151;
Best Local Similarity 100.0%; Pred. NO. 5.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTGGCGGAGTTGGGGGCT 21
Db 107 GCTGGCGGAGTTGGGGGCT 127

RESULT 9
LOCUS BI055204 151 bp mRNA linear EST 15-JUN-2001
DEFINITION PM2-GN0495-050201-001-905 GN0495 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI055204
VERSION BI055204.1 GI:14462734
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 151)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

AA434384
LOCUS zw31h1.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
IMAGE:770949 3' similar to gb:U14723 CLUSTERIN PRECURSOR (HUMAN);
RNA sequence.

ACCESSION AA434384.1 GI:2139298
VERSION AA434384
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 151)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie,
T., Waterston, R., and Wilson, R.
WashU-Merck EST Project 1997
Unpublished
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m3 fwd. ET from Amersham.

FEATURES
source
1..151
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5980822"
/db_xref="taxon:9606"
/clone="IMAGE:770949"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="PH10B (ampicillin resistant)"
/clone_lib="Soares ovary tumor NbHOT"
/note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTTACCATCTGAGTGGGACGCGGTTTCTTTTCTTTTCTTTT 3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."

BASE COUNT 32 a 27 c 56 g 36 t
ORIGIN
Query Match 100.0%; Score 21; DB 9; Length 151;
Best Local Similarity 100.0%; Pred. NO. 5.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTGGCGGAGTTGGGGGCT 21
Db 107 GCTGGCGGAGTTGGGGGCT 127

RESULT 9
LOCUS BI055204 151 bp mRNA linear EST 15-JUN-2001
DEFINITION PM2-GN0495-050201-001-905 GN0495 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI055204
VERSION BI055204.1 GI:14462734
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 151)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
MEDLINE
10737800
PUBMED
CONTACT: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-GN0495-
050201-001-905&t3=2001-02-05&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 148.
Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="GN0495"
/note="Organ: placenta normal; Vector: puc18; Site 1: SmaI
; Site 2: SmaI; A mini-library was made by cloning Patent
products derived from ORESTES PCR (U.S. Letters Patent
Application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

BASE COUNT 24 a 32 c 61 g 34 t
ORIGIN
Query Match 100.0%; Score 21; DB 12; Length 151;
Best Local Similarity 100.0%; Pred. NO. 5.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTGGCGGAGTTGGGGGCT 21
Db 61 GCTGGCGGAGTTGGGGGCT 81

RESULT 10
LOCUS BI040715 153 bp mRNA linear EST 14-JUN-2001
DEFINITION PM2-NT0232-120201-005-d02 NT0232 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI040715
VERSION BI040715.1 GI:14447341
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 153)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
MEDLINE

PUBMED
COMMENT

10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=PM2&t2=PM2-NT0232-
120201-005-402&t3=2001-02-12&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 34
High quality sequence stop: 153.

FEATURES
source
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone_lib="NT0232"
/notes="Organ: nervous tumor; Vector: puc18; Site 1: Sma1;
Site 2: Sma1; A mini-library was made by cloning products
derived from QRESUES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research).
Profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
17 a 36 c 67 g 33 t

BASE COUNT
17 a 36 c 67 g 33 t

ORIGIN

Query Match 100.0%; Score 21; DB 12; Length 153;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
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Db 35 GCTGGCGGAGTTGGGGCCT 55
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RESULT 11
BI467181
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
Homo sapiens
Homo sapiens (human)
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 157)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hiller, L., Marra, M., Pape, D., Wyllie, T., Martin, J., Blisstein, A.,
Schmitt, A., Theising, B., Ritter, E., Runko, I., Bennett, J., Cardenas
M., Gibbons, M., McCann, R., Cole, R., Tsagaris, R., Williams, T.,
Jackson, Y., and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished
Other_ESTRs: ic19a12.y3
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@bioph.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on

obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
High quality sequence stop: 142.
Location/Qualifiers
1..157
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/notes="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
Noti; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

BASE COUNT 35 a 28 c 56 g 38 t

ORIGIN

Query Match 100.0%; Score 21; DB 12; Length 157;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCGGAGTTGGGGCCT 21
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Db 104 GCTGGCGGAGTTGGGGCCT 124
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RESULT 12
BI040516
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
Homo sapiens
Homo sapiens (human)
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 159)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
PUBMED
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=PM2&t2=PM2-NT0232-
072021-004-c03&t3=2001-02-07&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 158.

FEATURES
source
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/organism="Homo sapiens"

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1. (bases 1 to 171)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.,
 Goldman, G.H., Carvalho, A.P., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.J.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?ti=IL0&t2=IL0-MT0215-281100-501-all&t3=2000-11-28&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 171.
 Location/Qualifiers
 1..171
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="MT0215"
 /note="Organ: marrow; Vector: puc18; Site_1: Smal; Site_2:
 Smal; A mini-library was made by cloning products derived
 from ORFESTES PCR (U.S. Letters Patent application No. 196
 ,716 - Ludwig Institute for Cancer Research) profiles
 into the puc 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."
 BASE COUNT 32 a 43 c 62 g 34 t
 ORIGIN
 Query Match 100.0%; Score 21; DB 10; Length 171;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTGGCGGAGTTGGGGGCT 21
 Db 21 GCTGGCGGAGTTGGGGGCT 41
 Search completed: January 21, 2004, 13:09:47
 Job time : 1739 secs